

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:41:41 ; Search time 1852.19 Seconds
(without alignments)
909.372 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactggggccctcc.....gtttctgcccagaatgctgc 104

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	104	100.0	722	14	BQ007008
C 2	104	100.0	1014	9	AL543083
C 3	103	99.0	248	14	T29839
C 4	86	82.7	581	9	AI242177
C 5	85	81.7	561	12	BG232086
C 6	61.4	59.0	660	9	AL575811

Result No.	Score	Query Match	Length	DB ID	Description
C 7	61.2	58.8	564	9	AA69697
C 8	60.8	56.5	562	9	AA207062
C 9	48.2	46.3	546	9	AA824594
C 10	34.8	33.5	136	17	B38591
C 11	32.6	31.3	691	9	AL110410
C 12	32.6	31.3	888	14	BQ232100
C 13	32.2	31.0	342	12	BF407522
C 14	31.8	30.6	876	17	CNS001Y
C 15	30.4	29.2	446	10	BB840094
C 16	30.4	29.2	452	9	AI286591
C 17	30.4	29.2	547	9	AA073604
C 18	30.4	29.2	679	14	BQ769691
C 19	30.4	29.2	711	14	BQ179477
C 20	30.4	29.2	721	17	AZ839536
C 21	30.4	29.2	792	13	BI454418
C 22	30.4	29.2	1038	14	BE963825
C 23	30.2	29.0	430	9	AA117760
C 24	29.8	28.7	768	17	BH027439
C 25	29.8	28.1	981	13	BM470874
C 26	29.2	28.1	266	10	BE020334
C 27	28.2	28.1	383	12	BE807705
C 28	28.2	28.1	460	10	BE611325
C 29	28.2	28.1	484	9	AJ003317
C 30	29.2	28.1	491	9	AL587755
C 31	29.2	28.1	506	10	AW704380
C 32	29.2	28.1	525	14	BM954069
C 33	28.2	28.1	885	12	BE873485
C 34	28.2	28.1	1021	17	CNS04LE6
C 35	29	27.9	509	17	AQ731196
C 36	29	27.9	589	9	AL682708
C 37	29	27.9	589	9	AL792732
C 38	29	27.9	604	9	AL678840
C 39	29	27.9	616	9	AL655516
C 40	29	27.9	638	9	AL642049
C 41	29	27.9	643	9	AL659308
C 42	29	27.9	658	17	AZ656161
C 43	29	27.9	690	29	AL632106
C 44	29	27.9	701	9	AL636546
C 45	29	27.9	1014	14	BQ942135

ALIGNMENTS

RESULT 1
BQ007008/c

LOCUS
DEFINITION
IMAGE:5846517 3', mRNA sequence.

ACCESSION
BQ007008

VERSION
BQ007008.1 GI:19731908

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 722)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

JOURNAL
COMMENT
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
The following repetitive elements were found in this cDNA
Sequence: 297-371, >(TAA)n\$Simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
Location/Qualifiers
1. 722
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5846517"
/clone_1lb="NCI_CGAP_E11"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTCAC.

BASE COUNT
204 a 162 c 164 g 190 t 2 others

Query Match
Best Local Similarity 100.0%; Score 104; DB 14; Length 722;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

RESULT 2
AL543083
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
Location/Qualifiers
1. 1014
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1002YE03"
/clone_1lb="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalised. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : <http://fulllength.invitrogen.com>

BASE COUNT
265 a 232 c 281 g 234 t 2 others

Query Match
Best Local Similarity 100.0%; Score 104; DB 9; Length 1014;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

RESULT 3
T29839
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

FEATURES
source
Location/Qualifiers
1. 248
/organism="Homo sapiens"
/db_xref="ATCC (inhost):107667"
/db_xref="taxon:9606"
/clone_1lb="Human Testis"
/note="Organ: testis"

BASE COUNT	63 a	65 c	60 g	57 t	3 others
ORIGIN					
Query Match	99.0%;	Score 103;	DB 14;	Length 248;	
Best Local Similarity	99.0%;	Pred. No. 3e-22;			
Matches 103;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
Db					
1	GAATTCAAACGTGGGGCCCTCCAGAACTACTACTGCGGCGCTACAGCTTTGATCCCTGACATCTG 60				
58	GAATTCAAACGTGGGGCCCTCCAGAACTACTACTGCGGCGCTACAGCTTTGATCCCTGACATCTG 117				
61	GAATCTGGAGACGAGGAGCGCTTTGCTGTCTGCGGCGAATGCTGC 104				
118	GAATCTNAGACGAGGAGCGCTTTGCTGTCTGCGGCGAATGCTGC 161				
RESULT 4					
LOCUS	AI242177/c	581 bp	mRNA	linear	EST 01-DEC-1998
DEFINITION	qblg08.x1 Soares-fetal_liver_spleen_infls.S1 Homo sapiens CDNA clone IMAGE:1851134 3' similar to gb:M0988 TUMOR NECROSIS FACTOR PRECURSOR (HUMAN); mRNA sequence.				
ACCESSION	AI242177				
VERSION	AI242177.1	GI:3837574			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 581)				
TITLE	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 1280 Std Error: 0.00 Seq primer: -400P from Glibco High quality sequence stop: 463. Location/Qualifiers				
FEATURES					
source	1..581				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:1851134"				
	/clone_lib="Soares-fetal_liver_spleen_infls.S1"				
	/sex="male"				
	/dev_stage="20 week-post conception fetus"				
	/lab_host="DH10 (ampicillin resistant)"				
	/note="Organ: Liver and Spleen; Vector: pTV3D (Pharmacia) with a modified polylinker; Site.1: Pac I; Site.2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' ACTGGAGAATTAATTAAGATCTTTTATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTV3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."				
BASE COUNT	179 a	130 c	135 g	137 t	
ORIGIN					
Query Match	82.7%;	Score 86;	DB 9;	Length 581;	
Best Local Similarity	90.2%;	Pred. No. 9.3e-17;			
Matches 92;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;	
Db					
3	ATTCAAACTGGGGCCCTCCAGAACTACTACTGCGGCGCTACAGCTTTGATCCCTGACATCTGGA 62				
579	AATTCAAACTGGGGCCCTCCAGAACTACTACTGCGGCGCTACAGCTTTGATCCCTGACATCTGGA 520				
63	ATCTGGAGACCGAGGAGCGCTTTGCTGTCTGCGGCGAATGCTGC 104				

DB	519	AFCGTGAGACCCAGGAGCCTTGGTCGTGCGCCACAGATCTCTGC	478
RESULT 5			
BG232086/c			
LOCUS	naf32e06.x1 Soares_NPBC	Homo sapiens cDNA clone IMAGE:4142698 3'	
DEFINITION	mRNA sequence.		
ACCESSION	BG232086		
VERSION	BG232086.1	GI:12727241	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 561)		
JOURNAL	NCI-CGAP htcp://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997) Tumor Gene Index Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov Tissue Procurement: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: info@image.lnl.gov Seq primer: -400P from Glbco High quality sequence stop: 482. Location/Qualifiers 1..561 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4142698" /clone_1lb="Soares_NPBC" /tissue_type="lymphocyte" /lab_host="DH10B (phage-resistant)" /note="Organ: blood; Vector: pTR7D-Pac; Site:1: NotI; Site:2: EcoRI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATTGTGAAGTGGAGCGGCCGCGGCTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. library is normalized; constructed in the laboratory of M. Bento Soares (University of Iowa)."		
BASE COUNT	176 a 125 c 129 g 131 t		
ORIGIN			
Query Match	81.7%; Score 85; DB 12; Length 561;		
Best Local Similarity	100.0%; Pred. No. 1,9e-16;		
Matches	85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	20 CAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATCTGGAGACCGAGGAG	79	
Dd	561 CAGAATCACTACAGGGCCCTACAGCTTTGATCCCTGACATCTGGAATCTGGAGACCGAGGAG	502	
OY	.80 CCTTGGTTCGGCCAGAAATGCTGC	104	
Db	501 CCTTGGTTCGGCCAGAAATGCTGC	477	
RESULT 6			
AL575811/c			
LOCUS	AL575811.LTI_NF006_P12	Homo sapiens cDNA clone CS001070Y015 3	
DEFINITION	prime, mRNA sequence.		
ACCESSION	AL575811.1	GI:12937341	

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 660)
TITLE	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES	location/Qualifiers
SOURCE	1..660
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="CSOD1070Y015"
	/clone_id="LRI_NFL006.Pl2"
	/tissue_type="Placenta"
	/note="Vector: pCMVSPORT 6; site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT	251 a 90 c 103 g 158 t 58 others
ORIGIN	
Query Match	59.0%; Score 61.4; DB 9; Length 660;
Best Local Similarity	68.9%; Pred. NO. 5.5e-09;
Matches	71; Conservative 8; Mismatches 24; Indels 0; Gaps 0;
OY	2 AATTCAACTGGGCGCTTCACACTCAGTGGGCGCTTATCCCGACATCTGG 61
DB	526 AATTCAACTTTTCTTCCTACATTCACCTCTTCTTATCCCTTATTCCTTTC 467
OY	62 AATCGAGACGAGGAGCGCTTTGGTTCTGGCGACAGATGTCGC 104
DB	466 AATCTTTATACCATTTATSTTTTCTTGTGSSAGATGTCGS 424
RESULT 7	
LOCUS	AA699697/C
DEFINITION	564 bp mRNA linear EST 19-DEC-1997
ACCESSION	z178f12.s1 Soares fetal liver spleen INTLS S1 Homo sapiens cDNA
VERSION	clone IMAGE:446927.3, similar to gb:M10988 TUMOR NECROSIS FACTOR
KEYWORDS	PRECURSOR (HUMAN);, mRNA sequence.
SOURCE	AA699697.1 GI:2703844
ORGANISM	EST.
	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 564)
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thelning, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.
TITLE	WashU-NCI human EST project
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is available royalty-free through LNL ; contact the

FEATURES	source
IMAGE Consortium (infoimage.llnl.gov) for further information. Seq primer: -40m13 fwd. 5' from Amersham High quality sequence stop: 397. Location/Qualifiers	1. 564 /organism="Homo sapiens" /db_xref="GDB:1351184" /db_xref="taxon:9606" /clone="IMAGE:446927" /clone_lib="Soares_fetal_liver_spleen_INFLS_S1" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /note="Organ: Liver and Spleen; Vector: p77Y3D (Pharmacia) with a modified polylinker. Site 1: Pac I; Site 2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INFES library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACGGAAGAATTATTAAGAATCTTTTATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p77Y3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	176 a 123 c 138 g 127 t
ORIGIN	
Query Match	58.8%; Score 61.2; DB 9; Length 564;
Best Local Similarity	85.1%; Pred. No. 6e-09;
Matches	80; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
OY	2 AATTCAACTGGGGCCCTCCAGACTCATCTGGGGCCCTACAGCTTTGATCCTGACA-TCGTG 60 Db 564 AATTCAACTGGGGCCCTCCAGACTCATCTGGGGCCCTACAGCTTATCCCGACATTCGTG 505 OY 61 GAATCTGGAGACGACGAGGAGCCTTGTGGTCTGACC 94 Db 504 ACATCTTGACACGACGAGGAGCCTTGTGTTCTGACC 471
RESULT 8 AA207062/c	562 bp mRNA linear EST 13-AUG-1997
LOCUS	zr87b03.s1 NCI CGAP GCBI Homo sapiens CDNA clone IMAGE:682637 3'
DEFINITION	similar to gp:M10988 TUMOR NECROSIS FACTOR PRECURSOR (HUMAN);, mRNA
ACCESSION	AA207062
VERSION	AA207062.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 562)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Seq primer: -40m13 fwd. from Amersham High quality sequence stop: 412. Location/Qualifiers
FEATURES	1. 562 /organism="Homo sapiens" /db_xref="GDB:5585957" /db_xref="taxon:9606" /clone="IMAGE:682637" /clone_lib="NCI-CGAP-GCBI" /tissue_type="germinal center B cell" /lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20⁺, 1D⁻),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TCGTACCATCTCAAGTGGAGGCGCCCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

Query Match	58.5%	Score 60.8;	DB 9;	Length 562;
Best Local Similarity	87.8%	Pred. No. 7.9e-09;		
Matches 65; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

Qy 31 GGGGCTACAGCTTGCATCCCTGACATCTGSATCTGGAGACCAGGAGCCTTTGGTTCT 90
||| | ||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 558 GGGCCTACCGGGCTGNATCCCTGACATCTNGAATCTGGAGACCAGGAGCCTTGCGTTCT 499

OY	91	GGCCAGAA	TGCTGC	104
Db	498	GGCCAGAA	TGCTGC	485

RESULT 9
AA824594/c

LOCUS	546 bp	mRNA	linear	EST 18-MAR-1998
DEFINITION	cc8d11.s1	NCI_CGAP_GCB1	Homo sapiens	CDNA clone IMAGE:1356509
	similar to	gb:MI0988	TUMOR NECROSIS FACTOR	PRECURSOR (HUMAN);, mRNA
	sequence:			

ACCESSION	AA824594	
VERSION	AA824594.1	GI:2896616
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
National Cancer Institute, Cancer genome Anatomy Project (CGAP).
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
1 (pages 1 to 546)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

JOURNAL
UNPUBLISHED (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.
Email: cgabps-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Ronaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnlnl.gov/brp/image/image.html
 Insert length: 614 Std Error: 0.00
 Seq primer: -40m13 fwd. ER from Amersham
 High quality sequence stop: 443.
 Location/Qualifiers

FEATURES
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3356309"
/clone_1ib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/node="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; 1st strand
cDNA was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),

```

provided by Dr. Louis M. Staundt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGCGCCGACATTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match	46.3%	Score 48.2	DB 9	length 546
Best Local Similarity	86.9%	Pred. No. 7.3e-05		
Matches 53; Conservative	0	Mismatches 8	Indels 0	Gaps 0

09 TTGATCCCTCAGCATCTGGATCTGGAGACCAGACCGACTTGTGGTTCTGGCCAGAAATCCTG 103
44 TTTGATCCCTCAGCATCTGGATCTGGAGACCAGACCGACTTGTGGTTCTGGCCAGAAATCCTG 103
Db 546 TTGATCCCGAACAATCTGGATCCGGAGACCCACGAGACCTTTGGTTCTGCCCAAGATTCTCG 487

QY	104	C	104
Db	486	C	486

RESULT 10
B38591

LOCUS	B38591	136 bp	DNA	linear	SSS 18-OCT-1997
DEFINITION	HS-1047-182-G12-MF.ab1	CYT	Human Genomic Sperm Library C Homo sapiens genomic clone	Plate-Cr 830 COL-24	ROW-N, DNA sequence.
ACCESSION	B38591				
VERSION	B38591.1	GI:2542843			

KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS

Eukaryota, Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo. 1 (bases 1 to 136)

Malanias, G.G., Zackrean, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.

TITLE	Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analyses of 20,000 Sequence Tagged Connectors
JOURNAL	Unpublished (1997)
COMMENT	Contact: Mahairas GG, Zackrone KD, Hood L

University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744

Tel: (206) 616-8744
 Fax: (206) 685-7301
 Email: kzackron@u.washington.edu
 Sequence Tagged Connector
 Plate: CT 830 row: N Column: 24
 Class: BAC ends

FEATURES

source

```

./organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-C7 830 Col-24 Row=N"
/clone_lib="C7 Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBelBacII; BAC Clones in
E-Coli DH10B"
BASE COUNT      32 a      33 c      35 g      34 t      2 others
ORIGIN

```

Query Match	33.5%	Score	34.8	DB	17	Length	136
Best Local	Similarly	62.1%	Pred. No.	0.73			
Matches	54	Conservative	0	Mismatches	33	Indels	0
						Gaps	0

07 AACCTGGGCTTCAGAACTCACTGGGGCTACAGCTTGTATCCCGACATCTGAACTCTG 67
11 11 111111 1111 11 111111 11 11 11 11 11
14 ACCGNGATCTCTAGATCGACTGCAGATGCAGCTTTCACTGTGGCTGCGGGCATGTG 73

RIKEN Integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carinici, P., Sugahara,
Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

Source

Location/Qualifiers

1. 446

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="E970004M24"

/clone_lib="RIKEN full-length enriched, 12 days embryo

whole body"

/tissue_type="whole body"

/dev_stage="12 days embryo"

/note="Vector: pSPOR1, Site_1: SalI; Site_2: NotI. This

clone is among a rearranged set of 15,247 clones from 11

embryo cDNA libraries (including preimplantation stage

embryos from unfertilized egg to blastocyst, embryonic

part of E7.5 embryos, extraembryonic part of E7.5 embryos

, and E12.5 female mesonephros/gonad) and one newborn

ovary cDNA library. Average insert size 1.5 kb. All

source libraries are cloned unidirectionally with Oligo(dT

)-Not primers. References include: (1) Genome-wide

expression profiling of mid-gestation placenta and embryo

using a 15,000 mouse developmental cDNA microarray, 2000,

Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)

Large-scale cDNA analysis reveals phased gene expression

patterns during preimplantation mouse development, 2000,

Development, 127: 1737-1749; (3) genome-wide mapping of

unselected transcripts from extraembryonic tissue of

7.5-day mouse embryos reveals enrichment in the t-complex

and under-representation on the X chromosome, 1998, Hum

Mol Genet 7: 1967-1978."

BASE COUNT 75 a 131 c 156 g 84 t

ORIGIN

Query Match

Best Local Similarity 29.2%; Score 30.4; DB 10; Length 446;

Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 8 AACGTGGGCTCCAGAACTCACTGGGCTTACAGCTTGATCCCTGACATCTGGAACTCG 67
DB 54 AGCGAGGCTTCGCCGACCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 113
QY 68 GAGACAGGAGGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 103
DB 114 GAGCTCAGGAGGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 149

Search completed: July 1, 2003, 22:11:21
Job time : 1860.19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 18:32:14 ; Search time 239, 837 Seconds
(without alignments)
976.530 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104
Sequence: 1 gaattcaactggggcctcc.....ggtctcgccagatctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: N_Geneseq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
25: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	104	100.0	104	21	AAZ99816	Cis-acting nucleot
2	104	100.0	787	20	AAZ20979	Human TNFalpha 3'U
3	104	100.0	1275	7	AAAN60558	Sequence encoding
4	104	100.0	1323	7	AAAN60363	Sequence encoding
5	104	100.0	1324	21	AAZ21085	Human low adenosin
6	104	100.0	1324	21	AAZ4963	Human adenosine re
7	104	100.0	1560	9	AAAN80219	Sequence of pE4 en
8	104	100.0	1585	7	AAAN60557	Sequence encoding
9	104	100.0	1606	7	AAAN60446	Sequence encoding

10	104	100.0	1606	17	AAAT15424	Human tumour necro
11	104	100.0	1643	17	AAAT1021	Human tumour necro
12	104	100.0	1643	24	ABR13195	Human tumour necro
13	104	100.0	2270	20	AAZ20983	Chimeric nucleic a
14	104	100.0	2570	20	AAZ20984	Chimeric nucleic a
15	104	100.0	3634	19	AAV39005	TNF-alpha gene use
16	104	100.0	3634	19	AAK09014	Tumour necrosis fa
17	104	100.0	3634	21	AAZ63770	Human TNF-alpha ge
18	104	100.0	3634	21	AAAO4340	Human tumour necro
19	104	100.0	7112	22	AAE6085	Lymphotoxin and tu
20	104	100.0	7112	22	AAE57450	Human tumour necro
21	104	100.0	16310	21	AAAF21086	Human low adenosin
22	104	100.0	16310	21	AAA4964	Human adenosine re
23	104	100.0	17634	21	AAZ1087	Human low adenosin
24	104	100.0	17634	21	AAZ1087	Human low adenosin
25	104	100.0	17634	21	AAA4965	Human adenosine re
26	104	100.0	17634	21	AAA4965	Human adenosine re
27	104	100.0	81800	24	ABK84756	Human CDNA differe
28	102.4	98.5	818	11	AAO04340	THP-1. Homo sapie
29	102.4	98.5	818	10	AAAN1035	XhoI - PstI sectio
30	102.4	98.5	1200	8	AAAT0072	Human anti-tumor p
31	102.4	98.5	1200	10	AAAN0969	Part of gene for a
32	102.4	98.5	1585	7	AAAN60527	Sequence encoding
33	102.4	98.5	1585	15	AAO58037	Tumour necrosis fac
34	102.4	98.5	1643	8	AAAT1307	Sequence encoding
35	91.8	88.3	815	8	AAAT0075	Human anti-tumor p
36	50	48.1	50	21	AAZ99815	Sequence of the st
37	43	41.3	43	21	AAZ99817	Cis-acting nucleot
38	33	31.7	51	21	AAZ99916	Sequence of the st
39	31.4	30.2	10240	19	AAV39007	Porcine TNF-alpha
40	30.2	29.0	2980	22	AAK6235	Human immune/haema
41	29.2	28.1	37664	22	AAK3781	Human immune/haema
42	29.2	28.1	61710	22	AAK3782	Human immune/haema
43	28.4	27.3	15650	22	ABAI5903	Human nervous syst
44	28.4	27.3	15650	22	ABAI5903	Human nervous syst
45	28.2	27.1	585	22	AAH11269	Human CDNA clone (

ALIGNMENTS

RESULT 1
AAZ99816 standard; RNA; 104 BP.
ID AAZ99816:
XX
AC AAZ99816:
XX
DT 12-JUL-2000 (first entry)
XX
AC 12-JUL-2000 (first entry)
XX
DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX
KW Cis-acting sequence; Intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
FN WO200014255-A1.
XX
PD 16-MAR-2000.
XX
PE 06-SEP-1999; 99WO-IL00483.
XX
PR 07-SEP-1998; 98IL-0126112.
XX
PR 26-OCT-1998; 98IL-0126757.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
XX WPI: 2000-257000/22.
XX
PT Regulation of gene expression by mRNA splicing is carried out using a

PT cis-acting nucleotide sequence controlled by phosphorylation of the
 XX alpha-subunit of eukaryotic initiation factor 2
 PS Claim 4: Page 15; 75pp; English.

CC The specification describes a cis-acting nucleotide sequence which is
 CC capable of removing introns from a precursor transcript encoded by a
 CC gene which harbours at least one cis-acting nucleotide sequence. This
 CC removal is effected during the production of mRNA of the gene, and
 CC depends on activation of a trans-acting factor which is an RNA-activated
 CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
 CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
 CC sequence, derived from the 3' untranslated region (3'UTR) of the human
 CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
 CC splicing of precursor transcripts encoded by that gene sensitive to the
 CC level of RNA-activated protein kinase (PKR) activity. The sequence can
 CC be used to transform host cells to regulate gene expression at the mRNA
 CC splicing level, for gene therapy, and to produce a recombinant
 CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
 CC protein) or industrially or agriculturally applicable protein. The
 CC present sequence represents a cis-acting nucleotide sequence of the
 CC invention.

SO Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 other;

Query Match 100.0%; Score 104; DB 21; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.2e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
 DB 1 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
 QY 61 GATCTGGAGACGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 104
 DB 61 GATCTGGAGACGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 104

RESULT 2
 AA220979
 ID AA220979 standard; DNA; 787 BP.

AC AA220979;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human TNFalpha 3'UTR.

XX TNFalpha: tumour necrosis factor alpha; apoptosis; inflammation;
 KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
 KW psoriasis; graft versus host disease; lupus erythematosus;
 KW diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO943840-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 12-JAN-1999; 99WO-US00637.
 XX
 PR 27-FEB-1998; 98US-0076316.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX
 PI Tatake RJ, Marlin SD, Barton RW;
 XX
 DR WPI; 1999-527630/44.
 XX
 XX A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
 PT promoter and an apoptosis-inducing Granzyme B polynucleotide
 XX
 PS Example 1; Page 60-61; 71pp; English.

XX This sequence represents a human TNFalpha (tumour necrosis factor alpha)
 CC 3'UTR (untranslated region). Chimeric nucleotides (AA220983, 220984)
 CC were constructed comprising at least one TNFalpha promoter enhancer
 CC region (AA220975-220987), a TNFalpha promoter (AA220972-220974), a DNA
 CC encoding the apoptosis-inducing Granzyme B protein (AA220982), and a
 CC TNFalpha 3'UTR sequence. TNFalpha is one of a number of
 CC cytokines produced by inflammatory cells. Upregulation and/or
 CC dysregulation of cytokines in inflamed tissue may be directly or
 CC indirectly responsible for exacerbation of chronic inflammatory
 CC diseases. Introduction of the chimeric nucleotide to activated
 CC inflammatory cells causes them to undergo apoptosis. Pharmaceutical
 CC compositions of the chimeric nucleotide may be useful for treating
 CC inflammatory disorders such as multiple sclerosis, Crohn's disease,
 CC ulcerative colitis, psoriasis, graft versus host disease, lupus
 CC erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing
 CC spondylitis, and in particular, rheumatoid arthritis. The use of such
 CC chimeric nucleotides offers simpler and cheaper long-term relief in
 CC comparison with existing conventional pharmaceutical and invasive surgery
 CC methods.

SO Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;

Query Match 100.0%; Score 104; DB 20; Length 787;
 Best Local Similarity 100.0%; Pred. No. 2.1e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
 DB 222 GAATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 281
 QY 61 GATCTGGAGACGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 104
 DB 282 GATCTGGAGACGAGGAGCCTTTGGTCTGGCCAGAAATGCTGC 325

RESULT 3
 AAN60558
 ID AAN60558 standard; DNA; 1275 BP.

AC AAN60558;
 XX
 DT 28-JUL-1991 (first entry)
 XX
 DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein
 DE Ser 69 in PAW731.
 XX
 KW Antitumour; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..474
 FT /tag= a
 XX
 PN WO8604606-A.
 XX
 PD 14-AUG-1986.
 XX
 PF 03-FEB-1986; 86WO-US00236.
 XX
 PR 07-FEB-1985; 85US-0698939.
 PR 19-OCT-1982; 82US-0435154.
 PR 15-APR-1983; 83US-0486162.
 PR 20-DEC-1983; 83US-0564224.
 PR 15-OCT-1984; 84US-0661026.
 PR 07-FEB-1985; 85US-0695934.
 XX
 PA (CETUS) CETUS CORP.
 XX
 PI Mark DF, Lin LS, Lu SDY, Wang AM;
 XX
 DR WPI; 1986-225458/34.

DR P-PSDB; AAP60656.
XX New synthetic muteins of human tumour necrosis factor protein -
PT are obtd. by direct mutagenesis and retain antitumour activity
XX
PS Disclosure; Fig 3a; 47pp; English.
XX
CC The sequence encoding TNF produced by the promyelocytic leukemia
CC cell line (HL-60, ATCC no. CCL240) has been cloned and expressed in
CC E. coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC the TNF sequence appears to be involved in disulphide linkages. The
CC placentors claim a novel synthetic mutein of a biologically active
CC hTNF protein, having at least one cysteine residue free from a
CC disulphide link and non-essential to the activity and having at
CC least one of the cysteine residues deleted or replaced by another AA.
CC Plasmid pAW731 (Ser 69) is claimed.
CC
SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;
Query Match 100.0%; Score 104; DB 7; Length 1275;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCTCCAGAACTCAGCTGGGGCTTGTATCCCTGACATCTG 60
DB 693 GAATTCAACTGGGGCTCCAGAACTCAGCTGGGGCTTGTATCCCTGACATCTG 752
QY 61 GAATCTGAGAGACGAGGAGCCTTGTGTTGGCCAGAAATGCTGC 104
DB 753 GAATCTGAGAGACGAGGAGCCTTGTGTTGGCCAGAAATGCTGC 796
RESULT 4
AAN60363
ID AAN60363 standard; DNA: 1323 BP.
AC AAN60363;
XX
DT 19-JUN-1991 (first entry)
XX
DE Sequence encoding human tumour necrosis factor.
XX hTNF; tumour; cancer; interferon; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..534
FT sig_peptide /*tag- a
FT 1..60
FT mat_peptide /*tag- b
FT 61..534
FT label= Secretory leader peptide
FT /*tag- c
XX
XX EPI68214-A.
XX
XX 15-JAN-1986.
XX
XX
XX 03-JUL-1985; 85EP-0304758.
XX
XX
XX 03-DEC-1984; 84US-0677454.
XX 05-JUL-1984; 84US-0627959.
XX 05-JUL-1984; 84US-0628059.
XX 05-JUL-1984; 84US-0628060.
XX 03-DEC-1984; 84US-0677156.
XX 03-DEC-1984; 84US-0677257.
XX 23-JUL-1984; 84US-0627959.
XX 03-DEC-1984; 84US-0677267.
XX
XX (GETH) GENENTECH INC.
XX
XX Aggarwal BB, Lee SH, Goeddel DY, Nedwin GE;
PI

XX
DR WPI: 1986-015483/03.
DR P-PSDB; AAP60417.
XX
XX Pure tumour necrosis factor and mutant forms - new DNA coding
PT sequences and transformed cells.
XX
PS Claim 20; Fig 10; 90pp; English.
XX
XX
CC Sequence encodes the pure human tumour necrosis factor, mutants of
CC which are covered by the claims. TNF and mutants are useful in
CC treating tumours, especially in tandem with interferon. The
CC encoding sequence may be used to create plasmid pTPXAPNF, allowing
CC transformation of an E. coli host for the expression of TNF.
CC
SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;
Query Match 100.0%; Score 104; DB 7; Length 1323;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCTCCAGAACTCAGCTGGGGCTTGTATCCCTGACATCTG 60
DB 750 GAATTCAACTGGGGCTCCAGAACTCAGCTGGGGCTTGTATCCCTGACATCTG 809
QY 61 GAATCTGAGAGACGAGGAGCCTTGTGTTGGCCAGAAATGCTGC 104
DB 810 GAATCTGAGAGACGAGGAGCCTTGTGTTGGCCAGAAATGCTGC 853
RESULT 5
AAF21085
ID AAF21085 standard; DNA: 1324 BP.
AC AAF21085;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2652.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX cancer; ss.
XX
XX Homo sapiens.
XX
XX W0200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US08020.
XX
XX 06-APR-1999; 99US-0127958.
XX
XX (UVEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX
XX Nyce JW;
XX
XX WPI: 2000-679539/66.
XX
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX
XX Disclosure; Page 887; 1592pp; English.
PS

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with the
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.

XX Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

XX Query Match 100.0%; Score 104; DB 21; Length 1324;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-25;
 XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGGCTTACAGCTTGATCCCGACATCTG 60
 DB |||||||
 DB 751 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGGCTTACAGCTTGATCCCGACATCTG 810
 CC |||||||

QY 61 GAATCTGAGACGACGAGGAGCTTTGGTTGTGCGCCAGAAATGCTGC 104
 DB |||||||
 DB 811 GAATCTGAGACGACGAGGAGCTTTGGTTGTGCGCCAGAAATGCTGC 854
 CC |||||||

RESULT 6

AAA34963
 ID AAA34963 standard; DNA; 1324 BP.

AC AAA34963;

DT 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:2652.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphotriolase; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impeded airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN WO200009525-A2.

XX 24-FEB-2000.

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1999; 98US-0095212.
 XX
 PA (UYBC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI: 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 PS
 XX Disclosure; Page 814-815; 1343pp; English.

XX The present invention describes a new composition comprising an
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
 CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC the ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing the
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680
 CC (AAA32313 to AAA3592) are specifically claimed ONs from the present
 CC invention. N.B. Sequences given in the disclosure of the present
 CC invention do not match up with their corresponding SEQ ID NO: sequences
 XX given in the sequence listing.

XX Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

XX Query Match 100.0%; Score 104; DB 21; Length 1324;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-25;
 XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGGCTTACAGCTTGATCCCGACATCTG 60
 DB |||||||
 DB 751 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGGCTTACAGCTTGATCCCGACATCTG 810
 CC |||||||

QY 61 GAATCTGAGACGACGAGGAGCTTTGGTTGTGCGCCAGAAATGCTGC 104
 DB |||||||
 DB 811 GAATCTGAGACGACGAGGAGCTTTGGTTGTGCGCCAGAAATGCTGC 854
 CC |||||||

RESULT 7

AAN80219
 ID AAN80219 standard; DNA; 1560 BP.

AC AAN80219;

DT 28-DEC-1990 (first entry)

XX Sequence of p64 encoding human tumour necrosis factor (TNF).

XX Lymphokine; antitumour; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 86..313 /tag= a

FT

FT mat_peptide 314..787
FT /*tag- b
XX
XX MO806625-A.
XX
XX 07-SEP-1988.
XX
XX 25-JAN-1988; 88WO-US00183.
XX
XX 26-FEB-1987; 87US-0019221.
XX
XX (CETU) CETUS CORP.
XX
XX Mark DF, Thomson JW, Lin LS, Yamamoto R;
XX WPI: 1988-271165/38.
XX P-PSDB: AAP80728.
XX
XX Human tumour necrosis factor mutelins -
XX having comparable biological activity with improved stability
XX and ease of purification
XX
XX Disclosure; Fig 1-1 to 1-2; 51pp; English.
XX
XX A human TNF protein which is modified from the sequence shown in
XX AAP80728, including naturally occurring allelic variants is claimed. Also
XX claimed are: recombinant DNA sequences encoding the protein (AAN80219)
XX and control sequences for expression; a vector; a transformed host cell;
XX a method of producing the protein by culturing the host cell;
XX pharmaceutical compsn. of the protein and a carrier and a method of
XX treating tumour burden with the compsn. The mutelins are capable of the
XX range of biological activities exhibited by native TNF but exhibit
XX improved stability and ease of purification.
XX
XX Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 other;
XX
XX Query Match 100.0%; Score 104; DB 9; Length 1560;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-25;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAATTCAAACGTGGGCTCCGAACTCAGTGGGCTTGTGATCCTGACATCTG 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1003 GAATTCAAACGTGGGCTCCGAACTCAGTGGGCTTGTGATCCTGACATCTG 1062
XX
XX 61 GAATCTGGAGACACAGGAGCCTTGTGTTGCGCCAGAAATGCTGC 104
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1063 GAATCTGGAGACACAGGAGCCTTGTGTTGCGCCAGAAATGCTGC 1106
XX
XX
XX RESULT 8
XX AAN60557
XX ID AAN60557 standard; DNA; 1585 BP.
XX
XX AC AAN60557;
XX
XX 28-JUL-1991 (first entry)
XX
XX Sequence encoding mature human tumour necrosis factor (hTNF) in pEA.
XX
XX Antitumour; anticancer; ss.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
XX CDS 86..313
XX FT /*tag- a
XX FT mat_peptide 314..787
XX FT /*tag- b
XX
XX MO80604606-A.
XX
XX 14-AUG-1986.
XX

PF 03-FEB-1986; 86WO-US00236.
XX
XX 07-FEB-1985; 85US-0698939.
XX 19-OCT-1982; 82US-0435154.
XX 15-APR-1983; 83US-0486162.
XX 20-DEC-1983; 83US-0564224.
XX 15-OCT-1984; 84US-0661026.
XX 07-FEB-1985; 85US-0695934.
XX
XX (CETU) CETUS CORP.
XX
XX Mark DF, Lin LS, Lu SDY, Wang AM;
XX WPI: 1986-225458/34.
XX P-PSDB: AAP60655.
XX
XX New synthetic mutelins of human tumour necrosis factor protein -
XX are obtd. by direct mutagenesis and retain antitumour activity
XX
XX Disclosure; Fig 1; 47pp; English.
XX
XX The sequence encoding TNF produced by the promyelocytic leukemia
XX cell line (HL-60, ATCC no. CCL240) has been cloned and expressed in
XX E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
XX the TNF sequence appears to be involved in disulphide linkages. The
XX patentors claim a novel synthetic mutelin of a biologically active
XX hTNF protein, having at least one cysteine residue free from a
XX disulphide link and non-essential to the activity and having at
XX least one of the cysteine residues deleted or replaced by another AA.
XX
XX Plasmid pMW731 (Ser 69) is claimed.
XX
XX Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;
XX
XX Query Match 100.0%; Score 104; DB 7; Length 1585;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-25;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAATTCAAACGTGGGCTCCGAACTCAGTGGGCTTGTGATCCTGACATCTG 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1003 GAATTCAAACGTGGGCTCCGAACTCAGTGGGCTTGTGATCCTGACATCTG 1062
XX
XX 61 GAATCTGGAGACACAGGAGCCTTGTGTTGCGCCAGAAATGCTGC 104
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1063 GAATCTGGAGACACAGGAGCCTTGTGTTGCGCCAGAAATGCTGC 1106
XX
XX
XX RESULT 9
XX AAN60446
XX ID AAN60446 standard; cDNA; 1606 BP.
XX
XX AC AAN60446;
XX
XX 07-AUG-1991 (first entry)
XX
XX Sequence encoding tumour necrosis factor (TNF).
XX
XX Anticancer agent; antitumour; antimetastatic; tumour necrosis factor;
XX ss.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
XX CDS 158..859
XX FT /*tag- a
XX FT
XX
XX MO8603751-A.
XX
XX 03-JUL-1986.
XX
XX 19-DEC-1985; 85WO-EP00721.
XX
XX 09-OCT-1985; 85US-0785847.
XX 21-DEC-1984; 84US-0684595.
XX

```
PR 09-OCT-1986; 86WO-US02133.
XX
XX (BIOJ ) BIOGEN NV.
PA (FIER/) FIERs W.C.
PA (ALIE/) ALLET B.
PA (BIOG-) BIOGEN INC.
XX
PI Fiers WC, Fransen LM, Tavernier JHL, Marmenout ALM;
PI VanDerHeyden J, Allet B, Washima EH;
XX
XX WPI, 1986-182891/28.
DR P-PSDB; AAP60531.
XX
XX Mammalian tumour necrosis factors - produced by culturing
PT pro-karyotic hosts transformed with recombinant DNA
XX
XX Example; Fig 9; 93pp; English.
XX
XX TNF-like polypeptides and compns. are produced by the fermentation
CC of host cells transformed with at least one DNA sequence which codes
CC for a mammalian TNF-like polypeptide operatively linked to an
CC expression control sequence in the transformed host.
XX
SQ Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;
Query Match 100.0%; Score 104; DB 7; Length 1606;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATCCCTGACATCTG 60
DB 1075 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATCCCTGACATCTG 1134
QY 61 GAATCTGAGAGACCAGGAGCCTTGGTTCTGGCCAGAAATGCTGC 104
DB 1135 GAATCTGAGAGACCAGGAGCCTTGGTTCTGGCCAGAAATGCTGC 1178

RESULT 10
AAT15424
ID AAT15424 standard; cDNA; 1606 BP.
XX
XX AAT15424;
AC
XX
XX 23-APR-1996 (first entry)
DE Human tumour necrosis factor cDNA clone p-hTNF-1.
XX
XX Tumour necrosis factor; TNF; phage T4; phage lambda; pl promoter;
KW antitumour; anticancer; antimetastatic; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 158..859
FT /tag- a
FT sig_peptide 158..385
FT /tag- b
FT mat_peptide 386..856
FT /*tag- c
XX
XX US5487984-A.
PN
XX
XX 30-JAN-1996.
PD
XX
XX 21-DEC-1984; 84US-0684595.
PF
XX
XX 20-DEC-1985; 85US-0811654.
PR 21-DEC-1984; 84US-0684595.
PR 09-OCT-1985; 85US-0785847.
XX
XX (BIOJ ) BIOGEN INC.
PA
XX
```

```
PI Allet B, Kawashima EH;
XX
XX WPI, 1996-105230/11.
DR P-PSDB; AAR88590.
XX
XX Prodn. of tumour necrosis factor - using recombinant DNA encoding
PT TNF under the control of T4 or lambda pl-T4 expression control
PT sequences.
XX
XX Example 9; Fig 9; 43pp; English.
XX
XX A cDNA clone (AAT15424), p-hTNF-1 (DSM 3160), codes for the human
CC tumour necrosis factor (hTNF) precursor (AAR88590). It was obtd.
CC by screening a human cDNA library with a fragment of mouse TNF
CC cDNA. The isolated cDNA may be linked to expression control
CC sequences from phage T4 or phage lambda (see AAT15402-05 and
CC AAT15425-26) for expression in host cells, esp. Escherichia coli,
CC and commercial-scale prodn. of recombinant TNF of use as an
CC antitumour, anticancer and antimetastatic agent.
XX
SQ Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;
Query Match 100.0%; Score 104; DB 17; Length 1606;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATCCCTGACATCTG 60
DB 1075 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATCCCTGACATCTG 1134
QY 61 GAATCTGAGAGACCAGGAGCCTTGGTTCTGGCCAGAAATGCTGC 104
DB 1135 GAATCTGAGAGACCAGGAGCCTTGGTTCTGGCCAGAAATGCTGC 1178

RESULT 11
AAT31021
ID AAT31021 standard; DNA; 1643 BP.
XX
XX AAT31021;
AC
XX
XX 26-SEP-1996 (first entry)
DE Human tumour necrosis factor cDNA clone HSTNFR.
XX
XX Gene therapy; hypoxia related enhancer element; HREE; Ischaemia;
KW reperfusion; promoter; tumour necrosis factor; TNF; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 153..854
FT /tag- a
XX
XX WO9620276-A1.
PN
XX
XX 04-JUL-1996.
PD
XX
XX 13-NOV-1995; 95WO-IB00996.
PF
XX
XX 23-DEC-1994; 94US-0365486.
PR
XX
XX (STRI ) SRI INT.
PA
XX
XX Bishopric NH, Green CJ, Laderoute KR, Murphy B;
PI Webster KA;
XX
XX WPI; 1996-321849/32.
DR P-PSDB; AAM00454.
XX
XX Chimeric gene contg. therapeutic gene linked to HREE - partic. for
PT expressing SOD etc. in hypoxic tissue to reduce tissue injury caused
PT by Ischaemia or reperfusion
```



```

XX PF 12-JAN-1999; 99WO-US00637.
XX XX
XX PR 27-FEB-1998; 98US-0076316.
XX XX
PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX PI Tataka RJ, MarlIn SD, Barton RW;
XX DR WPI: 1999-527630/44.
XX PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
XX promoter and an apoptosis-inducing Granzyme B polynucleotide
XX PS Claim 4; Fig 12; 71pp; English.
XX
CC This sequence represents chimeric nucleic acid -706TNFpGB3'UTR. This
CC comprises at least one TNFalpha (tumour necrosis factor alpha) promoter
CC enhancer region (AAZ20975-220978), a TNFalpha native promoter (AAZ20973),
CC a DNA encoding a truncated form of the apoptosis-inducing Granzyme B
CC protein (AAZ20982), and a TNFalpha 3'UTR (untranslated region)
CC sequence (AAZ20979). TNFalpha is one of a number of cytokines
CC produced by inflammatory cells. Upregulation and/or dysregulation
CC of cytokines in inflamed tissue may be directly or indirectly
CC responsible for exacerbation of chronic inflammatory diseases.
CC Introduction of this chimeric nucleotide to activated inflammatory cells
CC causes them to undergo apoptosis. Pharmaceutical compositions of this
CC chimeric nucleotide may be useful for treating inflammatory disorders
CC such as multiple sclerosis, Crohn's disease, ulcerative colitis,
CC psoriasis, graft versus host disease, lupus erythematosus,
CC insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis,
CC and in particular, rheumatoid arthritis. The use of such chimeric
CC nucleotides offers simpler and cheaper long-term relief, in comparison
CC with existing conventional pharmaceutical and invasive surgery methods.
XX
SQ Sequence 2270 BP; 556 A; 647 C; 545 G; 522 T; 0 other:

```

Query Match 100.0%; Score 104; DB 20; Length 2270;
 Best Local Similarity 100.0%; Pred. No. 2.8e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 GAATTCAAACCTGGGCGCTCCAGACTGAGCTGGGCGCTACAGTTGATCCCGACATCTG 60
DB 1705 GAATTCAAACCTGGGCGCTCCAGACTGAGCTGGGCGCTACAGTTGATCCCGACATCTG 1764
OY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1765 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1808

```

RESULT 14
 ID AAZ20984 standard; DNA; 2570 BP.
 AC AAZ20984;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Chimeric nucleic acid -1005TNFpGB3'UTR.
 XX
 KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
 KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
 KW psoriasis; graft versus host disease; lupus erythematosus;
 KW diabetes; ankylosing spondylitis; rheumatoid arthritis; promoter; ds.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Promoter 7..1033
 FT /tag= a
 FT /label= TNFalpha_promoter
 FT /note= "Human TNFalpha native promoter (AAZ20973)"

```

FT CDS 1040..1777
FT FT /*tag= b
FT FT /product= "Truncated Granzyme B"
FT FT /note= "Inactivating dipeptide absent"
FT FT 3'UTR 1790..2564
FT FT /*tag= c
FT FT /label= TNFalpha_3'UTR
XX
XX PN WO9943840-A1.
XX PD 02-SEP-1999.
XX
XX PF 12-JAN-1999; 99WO-US00637.
XX XX
XX PR 27-FEB-1998; 98US-0076316.
XX XX
PA (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX PI Tataka RJ, MarlIn SD, Barton RW;
XX DR WPI: 1999-527630/44.
XX PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
XX promoter and an apoptosis-inducing Granzyme B polynucleotide
XX PS Claim 4; Fig 13; 71pp; English.
XX
CC This sequence represents chimeric nucleic acid -1005TNFpGB3'UTR. This
CC comprises at least one TNFalpha (tumour necrosis factor alpha) promoter
CC enhancer region (AAZ20975-220978), a TNFalpha native promoter (AAZ20973),
CC a DNA encoding a truncated form of the apoptosis-inducing Granzyme B
CC protein (AAZ20982), and a TNFalpha 3'UTR (untranslated region)
CC sequence (AAZ20979). TNFalpha is one of a number of cytokines
CC produced by inflammatory cells. Upregulation and/or dysregulation
CC of cytokines in inflamed tissue may be directly or indirectly
CC responsible for exacerbation of chronic inflammatory diseases.
CC Introduction of this chimeric nucleotide to activated inflammatory cells
CC causes them to undergo apoptosis. Pharmaceutical compositions of this
CC chimeric nucleotide may be useful for treating inflammatory disorders
CC such as multiple sclerosis, Crohn's disease, ulcerative colitis,
CC psoriasis, graft versus host disease, lupus erythematosus,
CC insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis,
CC and in particular, rheumatoid arthritis. The use of such chimeric
CC nucleotides offers simpler and cheaper long-term relief, in comparison
CC with existing conventional pharmaceutical and invasive surgery methods.
XX
SQ Sequence 2570 BP; 639 A; 711 C; 650 G; 570 T; 0 other:

```

Query Match 100.0%; Score 104; DB 20; Length 2570;
 Best Local Similarity 100.0%; Pred. No. 2.8e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 GAATTCAAACCTGGGCGCTCCAGACTGAGCTGGGCGCTACAGTTGATCCCGACATCTG 60
DB 2005 GAATTCAAACCTGGGCGCTCCAGACTGAGCTGGGCGCTACAGTTGATCCCGACATCTG 2064
OY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 2065 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2108

```

RESULT 15
 ID AAV39005 standard; DNA; 3634 BP.
 AC AAV39005;
 XX
 DT 23-SEP-1998 (first entry)
 XX
 DE TNF-alpha gene used in the course of the invention.
 XX
 KW TNF-alpha; alteration; immunoreactivity; human cell;
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09826061-A2.
 XX
 PD 18-JUN-1998.
 XX
 PF 08-DEC-1997; 97WO-US22740.
 XX
 PR 01-DEC-1997; 97US-0982272.
 PR 09-DEC-1996; 96US-0032145.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Cantwell M, Kipps TJ, Sharma S;
 XX
 DR WPI; 1998-348521/30.
 XX
 PT Vectors containing accessory molecule ligand genes - used for
 PT altering immunoreactivity of cells, particularly for treatment of
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis
 XX
 PS Disclosure; Pages 107-108; 167pp; English.
 XX
 CC The present sequence represents a TNF-alpha gene. The sequence is
 CC used to exemplify the method of the invention. The specification
 CC describes a method for altering the immunoreactivity of human cells
 CC which comprises introducing a gene encoding an accessory molecule
 CC ligand (AML) into the cells so that the AML is expressed on the surface
 CC of the cells. Vectors containing the AML genes can be used in gene
 CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid
 CC arthritis. They can also be used for vaccination to produce immunity
 CC against a virus cell, bacteria, protein, fungus or neoplasia.
 CC
 XX
 SQ Sequence 3634 BP; 906 A; 959 C; 975 G; 794 T; 0 other;

Query Match 100.0%; Score 104; DB 19; Length 3634;
 Best Local Similarity 100.0%; Pred. No. 3.1e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGACTGAGGCTTGTGATCCCTGACATCTG 60
 Db 2808 GAATTCAACTGGGGCCTCCAGACTGAGGCTTGTGATCCCTGACATCTG 2867

QY 61 GAATCTGAGACCGAGGAGCCTTGGTTCTGGCCAGATGCTGC 104
 Db 2868 GAATCTGAGACCGAGGAGCCTTGGTTCTGGCCAGATGCTGC 2911

Search completed: July 1, 2003, 20:54:32
 Job time : 241.837 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 19:55:04 ; Search time 1383.13 Seconds

(without alignments)
2188.293 Million cell updates/sec

Title: US-09-801-371a-1

Perfect score: 104

Sequence: 1 gaattcaactggggcctcc.....ggttcctggccagaatgctgc 104

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_da:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rtd:*

36: em_htg_man:*

37: em_htg_vtl:*

38: em_sy:*

39: em_hlgo_hum:*

40: em_hlgo_mus:*

41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	400	11 G13533	G13533 SHGC-11076
2	104	100.0	1275	6 108430	108430 Sequence 5
3	104	100.0	1323	6 107953	107953 Sequence 6
4	104	100.0	1324	6 E00702	E00702 cDNA encod1
5	104	100.0	1324	6 103610	103610 Sequence 2
6	104	100.0	1465	6 104244	104244 Sequence 2
7	104	100.0	1585	6 A37272	A37272 Sequence 12
8	104	100.0	1585	6 104169	104169 Sequence 1
9	104	100.0	1585	6 104198	104198 Sequence 1
10	104	100.0	1585	6 108384	108384 Sequence 1
11	104	100.0	1585	6 108429	108429 Sequence 3
12	104	100.0	1585	6 HUMTNEFA	M10968 Human tumor
13	104	100.0	1606	6 107541	107541 Sequence 22
14	104	100.0	1643	6 AR146199	AR146199 Sequence
15	104	100.0	1643	9 HSTNFR	X01394 Human mRNA
16	104	100.0	1676	9 BC028148	BC028148 Homo sapi
17	104	100.0	3103	9 HUMTNEFX	M6331 Human tumor
18	104	100.0	3634	6 AR100270	AR100270 Sequence
19	104	100.0	3634	6 AR149925	AR149925 Sequence
20	104	100.0	3634	9 HSTNFA	X02910 Human gene
21	104	100.0	4830	9 AY066019	AY066019 Homo sapi
22	104	100.0	7112	6 AX100950	AX100950 Sequence
23	104	100.0	7112	6 AX100965	AX100965 Sequence
24	104	100.0	7112	9 HUMTNEFA	M16441 Human tumor
25	104	100.0	16310	9 HSTNFAFX	215026 Homo sapien
26	104	100.0	81800	9 HSY14768	Y14768 Homo sapien
27	104	100.0	100000	9 AP000505	AP000505 Homo sapi
28	104	100.0	135784	9 AL662847	AL662847 Human DNA
29	104	100.0	139399	9 AL662801	AL662801 Human DNA
30	104	100.0	184666	9 DJ201G24	AF129756 Homo sapi
31	104	100.0	212055	2 AP000899	AP000899 Homo sapi
32	102.4	98.5	817	6 A16444	A16444 Xho-PstI fr
33	102.4	98.5	817	6 E02109	E02109 DNA sequenc
34	102.4	98.5	1047	9 HSA249755	AJ249755 Homo sapi
35	102.4	98.5	1379	12 SYNTRFTRP	M35592 Synthetic h
36	102.4	98.5	1560	6 108863	108863 Sequence 3
37	73	70.2	1459	6 AF019963	AF019963 Paplo ham
38	59.8	57.3	349980	6 AX344556	AX344556 Sequence
39	58.2	56.0	349980	6 AX344568	AX344568 Sequence
40	58.2	56.0	349980	6 AX344569	AX344569 Sequence
41	49.6	47.7	2610	4 HSTNFA	M64087 Equus cabal
42	40.4	38.8	3200	4 RABTNF	M12846 Rabbit tymo
43	40.4	38.8	6577	4 RABTNF	M60340 Rabbit lym
44	35	33.7	209882	2 AC103554	AC103554 Rattus no
45	34.8	33.5	1071	10 CP077036	U77036 Cavia porce

ALIGNMENTS

RESULT 1

G13533

LOCUS SHGC-11076 Human Homo sapiens sts genomic, sequence tagged site.

DEFINITION G13533

ACCESSION G13533

VERSION G13533.1 GI:1129272

KEYWORDS STS.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 400)

AUTHORS Olivier M. and Cox D.R.

TITLE Unpublished, Olivier, M., Cox, D.R. (2000)

JOURNAL Unpublished (2000)

COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: CACTAGATTCATCAACCTGGGCGC
Primer B: GAGTAGAGCCCTAAGCTCCAC
STS size: 166
PCR profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/uL

Total Vol: 10 uL

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs derived from M10988 -- Unigene.

FEATURES

Location/Qualifiers

1..400

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="6"

/clone_11b="Human"

STS

primer_bind 210..231

primer_bind complement(356..375)

BASE COUNT 104 a 120 c 87 g 89 t

ORIGIN

Query Match 100.0%; Score 104; DB 11; Length 400;

Best Local Similarity 100.0%; Pred. No. 4e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGCGCTCCAGACTCACTGGGCGCTTGTGATCCCTGACATCTG 60

DB 216 GAATTCAACTGGGCGCTCCAGACTCACTGGGCGCTTGTGATCCCTGACATCTG 275

QY 61 GAATCTGGAGACCGAGGACCTTTGGTCTGTGCGCAGATGCTGC 104

DB 276 GAATCTGGAGACCGAGGACCTTTGGTCTGTGCGCAGATGCTGC 319

LOCUS 108430 1275 bp DNA linear PAT 02-DEC-1994

DEFINITION Sequence 5 from Patent WO 8604606.

ACCESSION 108430

VERSION 108430.1 GI:588860

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1275)

AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.

TITLE CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR

NECROSIS FACTOR PROTEINS

JOURNAL Patent: WO 8604606-A 5 14-AUG-1986;

FEATURES

Location/Qualifiers

1..1275

/organism="unknown"

BASE COUNT 297 a 357 c 309 g 312 t

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1275;

Best Local Similarity 100.0%; Pred. No. 4.3e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGCGCTCCAGACTCACTGGGCGCTTGTGATCCCTGACATCTG 60

DB 693 GAATTCAACTGGGCGCTCCAGACTCACTGGGCGCTTGTGATCCCTGACATCTG 752

QY 61 GAATCTGGAGACCGAGGACCTTTGGTCTGTGCGCAGATGCTGC 104

DB 753 GAATCTGGAGACCGAGGACCTTTGGTCTGTGCGCAGATGCTGC 796

LOCUS 107953 1323 bp DNA linear PAT 02-DEC-1994

DEFINITION Sequence 6 from Patent EP 0168214.

ACCESSION 107953

VERSION 107953.1 GI:589335

KEYWORDS

SOURCE

Unknown.

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1323)

AUTHORS Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.

Tumor necrosis factor, methods for its preparation, compositions

containing it, DNA encoding it and assay method using such DNA

Patent: EP 0168214-A2 6 15-JAN-1986;

JOURNAL

FEATURES

Location/Qualifiers

1..1323

/organism="unknown"

BASE COUNT 298 a 387 c 308 g 330 t

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1323;

Best Local Similarity 100.0%; Pred. No. 4.3e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGCGCTCCAGACTCACTGGGCGCTTGTGATCCCTGACATCTG 60

DB 750 GAATTCAACTGGGCGCTCCAGACTCACTGGGCGCTTGTGATCCCTGACATCTG 809

QY 61 GAATCTGGAGACCGAGGACCTTTGGTCTGTGCGCAGATGCTGC 104

DB 810 GAATCTGGAGACCGAGGACCTTTGGTCTGTGCGCAGATGCTGC 853

LOCUS 107953 1324 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding human tumor necrosis factor.

ACCESSION E00702

VERSION E00702.1 GI:2168979

KEYWORDS JP 1986040221-A/1.

SOURCE

ORGANISM

Homo sapiens

Human

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1324)

AUTHORS Barata,B.A., Debilsudo,B.G., San,H.R. and Guren,E.N.

TUMOR NECROTIC FACTOR

Patent: JP 1986040221-A 1 26-FEB-1986;

JOURNAL GENENTECH INC

OS homosaapiens

PN JP 1986040221-A/1

PD 26-FEB-1986

PF 05-JUL-1985 JP 1985149075

PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR
 05-JUL-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR
 03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454, PI BARA
 BUSHITAN AGAMARU, DEBITSDO BANNOOMAN GETSUDERU, PI
 PI GUREN EBAN NEDOUIN
 PC A61K35/12, A61K35/02, A61K35/14, A61K37/04, C07H21/02,
 PC C07H21/04,
 PC C12N15/00;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: cell-type=promyelocytes;
 CC *source: cell_line=HL-60;
 CC *source: clone=lamda42-4, lamda16-4;
 FH key Location/Qualifiers
 FT sig_peptide <1..61
 FT mat_peptide 62..532
 FT /product='tumor necrosis factor' FT CDS
 FT <1..535 /product='tumor necrosis factor' FT 3'UTR
 FT 536..>1324.
 Location/Qualifiers
 1..1324
 /organism='Homo sapiens'
 /db_xref='taxon:9606'
 298 a 387 c 308 g 331 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 4.3e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 751 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 810

Db 61 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 104
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 811 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 854

RESULT 5
 LOCUS 103610 1324 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 2 from Patent US 4650674.
 ACCESSION 103610
 VERSION 103610.1 GI:268632
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1324)
 AUTHORS Aggarwal, B.B. and Lee, S.He.
 TITLE Synergistic cytotoxic composition
 JOURNAL Patent: US 4650674-A 2 17-MAR-1997;
 Genentech, Inc.; So. San Francisco, CA
 FEATURES
 source Location/Qualifiers
 1..1324
 /organism='unknown'
 298 a 387 c 308 g 331 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 4.3e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 751 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 810

QY 61 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 104
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 104

Db 811 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 854
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6
 LOCUS 104244 1465 bp ss-DNA linear PAT 21-MAY-1993
 DEFINITION Sequence 2 from Patent US 4677197.
 ACCESSION 104244
 VERSION 104244.1 GI:268725
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1465)
 AUTHORS Lin, L.S. and Yamamoto, R.
 TITLE Purification method for tumor necrosis factor
 JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
 Cetus Corporation; Emeryville, CA
 FEATURES
 source Location/Qualifiers
 1..1465
 /organism='unknown'
 324 a 429 c 363 g 349 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1465;
 Best Local Similarity 100.0%; Pred. No. 4.3e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 883 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 942

QY 61 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 104
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 943 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 986

RESULT 7
 LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 12 from Patent WO9404196.
 ACCESSION A37272
 VERSION A37272.1 GI:2294369
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 1585)
 AUTHORS Vile, R.G. and Hart, I.R.
 TITLE TUMOUR THERAPY
 JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
 IMP CANCER RES TECH (GB)
 FEATURES
 source Location/Qualifiers
 1..1585
 /organism='unidentified'
 /db_xref='taxon:32644'
 352 a 473 c 389 g 371 t

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
 Best Local Similarity 100.0%; Pred. No. 4.3e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1003 GAATCAAACTGGGGCTCCAGAACTCACTGGGGCTTGAATCCTTGACATCTG 1062

QY 61 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 104
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1063 GAATCTGGAGACACAGGAGCCTTGTGTCGGCCAGATGCTGC 1106

```

RESULT 8
LOCUS 104169
DEFINITION Sequence 1 from Patent US 4677063.
ACCESSION 104169
VERSION 104169.1 GI:268716
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
Arsdell,J.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677063-A 1 30-JUN-1987;
FEATURES
source
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 9
LOCUS 104198
DEFINITION Sequence 1 from Patent US 4677064.
ACCESSION 104198
VERSION 104198.1 GI:268719
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Van Arsdell,J.N.
and Lin,L.S.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677064-A 1 30-JUN-1987;
FEATURES
source
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 10
LOCUS 108384
DEFINITION Sequence 5 from Patent WO 8602381.
ACCESSION 108384
VERSION 108384.1 GI:588904
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
Arsdell,J.N.
TITLE HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;
FEATURES
source
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 11
LOCUS 108429
DEFINITION Sequence 3 from Patent WO 8604606.
ACCESSION 108429
VERSION 108429.1 GI:588859
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 3 14-AUG-1986;
FEATURES
source
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 12
LOCUS HUMTNFAA
DEFINITION Human tumor necrosis factor (TNF) mRNA.
ACCESSION M10988
VERSION M10988.1 GI:339737
KEYWORDS
SOURCE Human cDNA to mRNA, clone pE4.

```

```

DEFINITION Sequence 5 from Patent WO 8602381.
ACCESSION 108384
VERSION 108384.1 GI:588904
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
Arsdell,J.N.
TITLE HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;
FEATURES
source
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 11
LOCUS 108429
DEFINITION Sequence 3 from Patent WO 8604606.
ACCESSION 108429
VERSION 108429.1 GI:588859
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
CYSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 3 14-AUG-1986;
FEATURES
source
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 12
LOCUS HUMTNFAA
DEFINITION Human tumor necrosis factor (TNF) mRNA.
ACCESSION M10988
VERSION M10988.1 GI:339737
KEYWORDS
SOURCE Human cDNA to mRNA, clone pE4.

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1585)
AUTHORS Wang, A.M., Creasey, A.A., Ladner, M.B., Lin, L.S., Strickler, J., Van Arsdale, J.N., Yamamoto, R. and Mark, D.F.
TITLE Molecular cloning of the complementary DNA for human tumor necrosis factor

JOURNAL Science 228 (4696), 149-154 (1985)
MEDLINE 85142190
PUBMED 3856324

FEATURES
source
Location/Qualifiers
1..1585
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
1..1585
/gene="TNFA"
86..787
/gene="TNFA"
/note="tumor necrosis factor"
/codon_start=1
/protein_id="AA61198.1"
/db_xref="GI:339738"
/db_xref="GDB:G00-120-441"
/translation="MSTESMIRDELAEALPKKGGPOGSRRLFLSLFSLIYAGA
TTFLLHFGVIGVGPRESRDLISLPLAQAVRSSRPSDPAVAVANPAEGOL
QMLNRANMLLANGVELRDQVLVPSGLILITSVLPKGGCPSTHVLTHITSLIA
VSTQKVNLSIAKSPCQRTPEGAERAPWEPIYLGVAFLKGRSLSEINRPPYL
DFAESQVFFGIATL"

BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN Chromosome 6p21.3.

Query Match 100.0%; Score 104; DB 9; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTACACAGCTTGTGATCCCTGACATCTG 60
|||||
Db 1003 GAATCAAACTGGGGCTCCAGAACTACACAGCTTGTGATCCCTGACATCTG 1062

QY 61 GAATCTGAGACAGGAGGCTTGTGTCGCGAGATCTGC 104
|||||
Db 1063 GAATCTGAGACAGGAGGCTTGTGTCGCGAGATCTGC 1106

RESULT 13
LOCUS 107541 1606 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 22 from Patent EP 0313104.
ACCESSION 107541
VERSION 107541.1 GI:590445
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1606)
AUTHORS Fiers, W.C., Franzen, L.M., Tavernier, J.H.L., Marmerout, A.L.M., van der Heyden, J., Allet, B. and Kawahima, E.H.
TITLE Purification, production and use of tumor necrosis factors
JOURNAL Patent: EP 0313104-A2 22-26-APR-1989;
FEATURES
source
Location/Qualifiers
1..1606
/organism="unknown"

BASE COUNT 357 a 494 c 394 g 361 t

Query Match 100.0%; Score 104; DB 6; Length 1606;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTACACAGCTTGTGATCCCTGACATCTG 60
|||||
|||||

Db 1075 GAATCAAACTGGGGCTCCAGAACTACACAGCTTGTGATCCCTGACATCTG 1134

QY 61 GAATCTGAGACAGGAGGCTTGTGTCGCGAGATCTGC 104
|||||

Db 1135 GAATCTGAGACAGGAGGCTTGTGTCGCGAGATCTGC 1178

RESULT 14
LOCUS ARI46199 1643 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 36 from patent US 6218179.
ACCESSION ARI46199
VERSION ARI46199.1 GI:15109388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1643)
AUTHORS Webster, K.A., Bishopric, N.H., Murphy, B., Laderoute, K.R. and Green, C.J.
TITLE Tissue specific hypoxia regulated constructs
JOURNAL Patent: US 6218179-A 36-17-APR-2001;
FEATURES
source
Location/Qualifiers
1..1643
/organism="unknown"

BASE COUNT 370 a 495 c 398 g 380 t

Query Match 100.0%; Score 104; DB 6; Length 1643;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTACACAGCTTGTGATCCCTGACATCTG 60
|||||
Db 1070 GAATCAAACTGGGGCTCCAGAACTACACAGCTTGTGATCCCTGACATCTG 1129

QY 61 GAATCTGAGACAGGAGGCTTGTGTCGCGAGATCTGC 104
|||||
Db 1130 GAATCTGAGACAGGAGGCTTGTGTCGCGAGATCTGC 1173

RESULT 15
LOCUS HSTNR 1643 bp mRNA linear PRI 21-MAR-1995
DEFINITION Human mRNA for tumor necrosis factor.
ACCESSION X01394
VERSION X01394.1 GI:37219
KEYWORDS tumor necrosis factor.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1643)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 1643)
JOURNAL Penica, D., Nedwin, G.E., Hayflick, J.S., Seeburg, P.H., Derynck, R., Palladino, M.A., Kohr, W.J., Aggarwal, B.B. and Goeddel, D.V.
TITLE Human tumor necrosis factor: precursor structure, expression and homology to lymphotoxin
JOURNAL Nature 312 (5996), 724-729 (1984)
MEDLINE 85086244
PUBMED 6392892
REFERENCE 2 (bases 1 to 1643)
AUTHORS Shirai, T., Yamaguchi, H., Ito, H., Todd, C.W. and Wallace, R.B.
TITLE Cloning and expression in Escherichia coli of the gene for human tumor necrosis factor
JOURNAL Nature 313 (6005), 803-806 (1985)
MEDLINE 85137898
PUBMED 3883195
COMMENT In the genomic sequence from ref [2] the mature protein starts with Ser (position 387 in this cDNA sequence).
FEATURES
source
Location/Qualifiers
1..1643
/organism="Homo sapiens"
/db_xref="taxon:9606"

CDS

153..854
 /note="TNF precursor"
 /codon_start=1
 /protein_id="CAA25650.1"
 /db_xref="GI:37220"
 /db_xref="SWISS-PROT:P01375"
 /translation="WSTESMINDVELAEALPKKGGPGGSRRLFLSLFSLIVAGA
 TTLFLHLHGVIGPQREFFPRDLISPLAQAVRSSRTPSDKPYAHVYANPOAEGOL
 QMLNRRANALLANGVELRDNOIVPSEGLIYISOVLFGGCGCPSTHYLLTHTISRIA
 VSYOTKVNILSAIKSPQCQREPEGAEAAPWYEPYILGGVFQLEKGDRLSAEINRPDYL
 DEAESGOYFFGIIL"
 153..380
 /note="putative"
 mat_peptide 381..851
 /product="mature TNF (aa 1-157)"
 mlsc_feature 1630..1635
 /note="put. polyadenylation signal"
 BASE COUNT 370 a 495 c 398 g 380 t
 ORIGIN

Query Match

Best Local Similarity 100.0%; Score 104; DB 9; Length 1643;
 Pred. No. 4.3e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGCGCTCCAGACTCACTGGGCGCTACAGCTTGTGATCCTGACATCTG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1070 GAATTCAAACTGGGCGCTCCAGACTCACTGGGCGCTACAGCTTGTGATCCTGACATCTG 1129
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 GAATCTGGAGACCAGGAGCCTTGTGTCTGTGGCCAGAAATGCTGC 104
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1130 GAATCTGGAGACCAGGAGCCTTGTGTCTGTGGCCAGAAATGCTGC 1173
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: July 1, 2003, 21:27:26

Job time : 1389.13 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:43:24 ; Search time 50.2313 Seconds
(without alignments)
634.950 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104
Sequence: 1 gaattcaacacggggcctcc.....gtctcggccgaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCtUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	1643	US-08-880-342-36	Sequence 36, Appl
2	104	100.0	1643	US-09-505-250-4	Sequence 4, Appl
3	104	100.0	3634	US-09-166-186-1	Sequence 1, Appl
4	104	100.0	3634	US-09-313-932-1	Sequence 1, Appl
5	104	100.0	3634	US-09-109-663-34	Sequence 34, Appl
6	28	26.9	28720	US-09-341-587-7	Sequence 7, Appl
7	26.4	23.4	3181	US-08-655-086-1	Sequence 1, Appl
8	25.8	24.8	3889	US-09-484-970B-39	Sequence 39, Appl
9	25.8	24.8	4031	US-08-159-784-1	Sequence 1, Appl
10	25.6	24.6	642	US-09-328-111-82	Sequence 82, Appl
11	25.6	24.6	2634	US-08-911-853-30	Sequence 30, Appl
12	25.6	24.6	2634	US-09-479-409-30	Sequence 30, Appl
13	25.6	24.6	2634	US-09-479-453-30	Sequence 30, Appl
14	25.6	24.6	17612	US-08-911-853-29	Sequence 29, Appl
15	25.6	24.6	17612	US-09-479-409-29	Sequence 29, Appl
16	25.6	24.6	17612	US-09-479-453-29	Sequence 29, Appl
17	25.4	24.4	220	US-09-263-933-22	Sequence 22, Appl
18	25.4	24.4	604	US-09-068-880-1	Sequence 1, Appl
19	25.4	24.4	1026	US-09-068-880-14	Sequence 14, Appl
20	25.4	24.4	1289	US-09-247-155-138	Sequence 138, App
21	25.4	24.4	1467	US-09-330-317B-17	Sequence 17, Appl
22	25.4	24.4	1467	US-09-808-589A-17	Sequence 17, Appl
23	25.4	24.4	1956	US-08-867-352-20	Sequence 20, Appl
24	25.4	24.4	4145	US-08-314-917-1	Sequence 1, Appl
25	25.4	24.4	4145	US-08-265-046-1	Sequence 1, Appl
26	25.4	24.4	4145	US-08-465-522-1	Sequence 1, Appl
27	25.4	24.4	4145	PCr-US93-11401-1	Sequence 1, Appl

28	25.4	24.4	4145	5	PCr-US95-07849-1	Sequence 1, Appl
29	25.4	24.4	4951	2	US-08-752-307B-1	Sequence 1, Appl
30	25.4	24.4	4951	4	US-09-707-802-1	Sequence 1, Appl
31	25.4	24.4	4951	4	US-09-991-326-1	Sequence 1, Appl
32	25.4	24.4	7076	4	US-09-837-863-20	Sequence 20, Appl
33	25.4	24.4	7076	4	US-09-837-863-21	Sequence 21, Appl
34	25.4	24.4	7092	4	US-09-837-863-19	Sequence 19, Appl
35	25.4	24.4	7092	4	US-09-837-863-22	Sequence 22, Appl
36	25.4	24.4	7208	3	US-09-166-186-107	Sequence 107, App
37	25.4	24.4	7208	4	US-09-313-932-107	Sequence 107, App
38	25.4	24.4	7573	4	US-09-837-863-27	Sequence 27, Appl
39	25.4	24.4	8299	1	US-08-462-014-2	Sequence 2, Appl
40	25.4	24.4	8299	3	US-08-923-137-3	Sequence 3, Appl
41	25.4	24.4	8299	4	US-08-973-334-5	Sequence 5, Appl
42	25.4	24.4	8299	4	US-09-563-989A-5	Sequence 5, Appl
43	25.4	24.4	8299	4	US-09-663-933-1	Sequence 1, Appl
44	25.4	24.4	13910	4	US-09-263-933-8	Sequence 8, Appl
45	25.4	24.4	13910	4	US-09-263-933-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0860
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE: TNF CDNA HSTNFR (EMBL Accession
INDIVIDUAL ISOLATE: #X01394)
INDIVIDUAL ISOLATE: #X01394)
FEATURE:
NAME/KEY: CDS
LOCATION: 153..851
US-08-880-342-36

Query Match 100.0%; Score 104; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 5.5e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATGATCCCTGACATCTG 1129
QY 61 GAATCTGAGACGAGGAGCCTTTGGTCTGGGCCAAGATGCTGC 104
DB 1130 GAATCTGAGACGAGGAGCCTTTGGTCTGGGCCAAGATGCTGC 1173

RESULT 2

US-09-505-250-4
Sequence 4, Application US/09505250A
Patent No. 6329148
GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
APPLICANT: Kao, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1643
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (153)...(854)
US-09-505-250-4

Query Match 100.0%; Score 104; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 5.5e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATGATCCCTGACATCTG 1129
QY 61 GAATCTGAGACGAGGAGCCTTTGGTCTGGGCCAAGATGCTGC 104
DB 1130 GAATCTGAGACGAGGAGCCTTTGGTCTGGGCCAAGATGCTGC 1173

RESULT 3

US-09-166-186-1
Sequence 1, Application US/09166186A
Patent No. 6080580
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- α EXPRESSION
FILE REFERENCE: ISPH-0322
CURRENT APPLICATION NUMBER: US/09/166,186A
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 250
SEQ ID NO 1

LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
FEATURE:
NAME/KEY: exon
LOCATION: (615)..(981)
FEATURE:
NAME/KEY: intron
LOCATION: (982)..(1588)
FEATURE:
NAME/KEY: exon
LOCATION: (1589)..(1634)
FEATURE:
NAME/KEY: intron
LOCATION: (1635)..(1821)
FEATURE:
NAME/KEY: exon
LOCATION: (1822)..(1869)
FEATURE:
NAME/KEY: intron
LOCATION: (1870)..(2070)
FEATURE:
NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Maylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

Query Match 100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATGATCCCTGACATCTG 60
DB 2808 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCCTTATGATCCCTGACATCTG 2867
QY 61 GAATCTGAGACGAGGAGCCTTTGGTCTGGGCCAAGATGCTGC 104
DB 2868 GAATCTGAGACGAGGAGCCTTTGGTCTGGGCCAAGATGCTGC 2911

RESULT 4

US-09-313-932-1
Sequence 1, Application US/09313932A
Patent No. 6228642
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
FILE REFERENCE: ISPH-0356
CURRENT APPLICATION NUMBER: US/09/313,932A

```

; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (1870)..(2070)
; NAME/KEY: exon
; LOCATION: (2171)..(3811)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes:
; TITLE: structure, homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
; US-09-313-932-1

Query Match          100.0%; Score 104; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7,1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 2808 GAATTCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867
QY 61 GAATCTGGAGACACAGGAGCCTTGTGCTTGCGCCAGAAATGCTGC 104
DB 2868 GAATCTGGAGACACAGGAGCCTTGTGCTTGCGCCAGAAATGCTGC 2911

RESULT 5
US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
; APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-301
```

```

; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: OTHER INFORMATION: TNF(alpha) cDNA
; US-09-109-663-34

Query Match          100.0%; Score 104; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7,1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 60
DB 2808 GAATTCAAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 2867
QY 61 GAATCTGGAGACACAGGAGCCTTGTGCTTGCGCCAGAAATGCTGC 104
DB 2868 GAATCTGGAGACACAGGAGCCTTGTGCTTGCGCCAGAAATGCTGC 2911

RESULT 6
US-09-341-587-7/c
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRcR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; EARLIER FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-341-587-7

Query Match          26.9%; Score 28; DB 4; Length 28720;
Best Local Similarity 58.3%; Pred. No. 3;
Matches 49; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AATTCAACTGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTTGATCCCTGACATCTG 61
DB 14762 AATTTGAAGAGGGTCTTGAAGAGAGAGAGGGGACATCTCATTTGTACACAGTCTGAGG 14703
QY 62 AATCTGAGACACAGGAGCCTTTG 85
DB 14702 TATTTTGTACACAGGAATCATCTG 14679

RESULT 7
US-08-655-086-1
; Sequence 1, Application US/08655086
; Patent No. 5821089
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOTT A.
; APPLICANT: BUECHTER, DOUGLAS
; APPLICANT: ZHANG, GUANGHUI
; APPLICANT: CONNOLLY, KEVIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DILMORTH & BARRESE
; STREET: 333 EARLE OVINGTON BOULEVARD
```

CITY: UNIONDALE
STATE: NY
COUNTRY: US
ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,086
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S.
REGISTRATION NUMBER: 32,063
REFERENCE/DOCKET NUMBER: 203-1632
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-228-8484
TELEFAX: 516-228-8516
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cdna
US-08-655-086-1

Query Match 25.4%; Score 26.4; DB 1; Length 3181;
Best Local Similarity 57.1%; Pred. No. 5.5;
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 8 AACCTGGGCGCTCCAGAACTCACTGGGCGCTTACAGCTTTGATCCCTGACATCTGGAATCTG 67
DB 1317 ACCGAGGTCTTCCGCGACCCCGCTGCTGCTCTGCAAGATGAGAGAGCTG 1376

OY 68 GAGACCAGGAGCGCTTTGGTCTG 91
DB 1377 GAGCTCAGGAGCCCTCGCCCTG 1400

RESULT 8
US-09-484-970B-39/c
Sequence 39, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 39
LENGTH: 3889
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 251277.1CB1
US-09-484-970B-39

Query Match 24.8%; Score 25.8; DB 4; Length 3889;
Best Local Similarity 60.9%; Pred. No. 9.4;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 30 TGGGGCCCTACCTTTGATCCTGACATCTGGAATCTGAGACAGGAGCGCTTTGGTTC 89
DB 625 TGGCCCTGTGCGCAAGTTCCTGACCCATGAGCCAGGAGGAGCACTGCGTCTTGGTTC 566

OY 90 TGGCCAGAA 98
DB 565 CGGTCAGCA 557

RESULT 9
US-08-159-784-1
Sequence 1, Application US/08159784
Patent No. 5643783
GENERAL INFORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555x
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00246/170001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4031
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-159-784-1

Query Match 24.8%; Score 25.8; DB 1; Length 4031;
Best Local Similarity 54.8%; Pred. No. 9.6;
Matches 51; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY 11 TGGGGCGCTCCAGAACTCACTGGGCGCTTACAGCTTTGATCCCTGACATCTGGAATCTGAG 70
DB 2513 TGGGCCCTGCTGCGGCGGCGGCGGCAATTTCCCATTTGACTCTTCCACTGGAAGCGGAA 2572

OY 71 ACCAGGAGCGCTTTGGTCTTGGCCAGCAATGCTG 103
DB 2573 TGAAGGGGAGCAAGGAGGAGCGAGGAGGAGCTG 2605

RESULT 10
US-09-328-111-82/c
Sequence 82, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.

APPLICANT: Dertl, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 82
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-111-82

Query Match 24.6%; Score 25.6; DB 4; Length 642;
Best Local Similarity 87.5%; Pred. No. 6.3;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 47 ATCCCTGACATCTGGAATCTGGAGCCAGGGA 78
DB 413 ATCACTGACATCTGGAATCTGGAGCCAGGGA 382

RESULT 11
US-08-911-853-30/C
Sequence 30, Application US/08911853
Patent No. 6048710
GENERAL INFORMATION:
APPLICANT: Gerritse, Gijbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,853
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,092
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-911-853-30

Query Match 24.6%; Score 25.6; DB 3; Length 2634;

Best Local Similarity 54.2%; Pred. No. 9.8;
Matches 52; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 8 AACTGGGGCTCCAGAACTCACTGGGCTTACAGTTTGATCCCTGACATCTGGAATCTG 67
DB 317 ACCTGGGGCTCCAGAACTCACTGGGCTTACAGTTTGATCCCTGACATCTGGAATCTG 258
QY 68 GAGACAGAGAGAGCTTGTCTGTGCGCCAGAAATGCTG 103
DB 257 TCGACCTGGGGCTCCAGAACTCACTGGGCTTACAGTTTGATCCCTGACATCTGGAATCTG 222

RESULT 12
US-09-479-409-30/C
Sequence 30, Application US/09479409
Patent No. 6225106
GENERAL INFORMATION:
APPLICANT: Gerritse, Gijbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,409
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-409-30

Query Match 24.6%; Score 25.6; DB 4; Length 2634;
Best Local Similarity 54.2%; Pred. No. 9.8;
Matches 52; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 8 AACTGGGGCTCCAGAACTCACTGGGCTTACAGTTTGATCCCTGACATCTGGAATCTG 67
DB 317 ACCTGGGGCTCCAGAACTCACTGGGCTTACAGTTTGATCCCTGACATCTGGAATCTG 258
QY 68 GAGACAGAGAGAGCTTGTCTGTGCGCCAGAAATGCTG 103
DB 257 TCGACCTGGGGCTCCAGAACTCACTGGGCTTACAGTTTGATCCCTGACATCTGGAATCTG 222

RESULT 13
US-09-479-453-30/C
Sequence 30, Application US/09479453
Patent No. 6313283
GENERAL INFORMATION:

```

; APPLICANT: Gerritse, Gijtsbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gjalster, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-479-453-30

Query Match      24.6%; Score 25.6; DB 4; Length 2634;
Best Local Similarity 54.2%; Pred. No. 9,8;
Matches 52; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY      8 AACTGGGGCCCTCCAGAACTGAGTGGGCTTACAGCTTGATCCCGATCGGAAATCG 67
DB      317 ACCCTGGGGCCCTGGTGCATCTCGGGCGGGAAGGGGTTGAACGACGAGTCGAAATCC 258
QY      68 GAGACGAGGAGACCTTTGGTCTGCGCCAGAAATCGT 103
DB      257 TCGACCTGGGGCGGAGATGCTTTCGCGCCAGTGGCGG 222

RESULT 14
US-08-911-853-29/c
; Sequence 29, Application US/08911853
; Patent No. 6048710
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijtsbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,853
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,092
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gjalster, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17612 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-911-853-29

Query Match      24.6%; Score 25.6; DB 3; Length 17612;
Best Local Similarity 54.2%; Pred. No. 18;
Matches 52; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY      8 AACTGGGGCCCTCCAGAACTGAGTGGGCTTACAGCTTGATCCCGATCGGAAATCG 67
DB      4732 ACCCTGGGGCCCTGGTGCATCTCGGGCGGGAAGGGGTTGAACGACGAGTCGAAATCC 4673
QY      68 GAGACGAGGAGACCTTTGGTCTGCGCCAGAAATCGT 103
DB      4672 TCGACCTGGGGCGGAGATGCTTTCGCGCCAGTGGCGG 4637

RESULT 15
US-09-479-409-29/c
; Sequence 29, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijtsbert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gjalster, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-845-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17612 base pairs
; TYPE: nucleic acid
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:48:50 ; Search time 137.252 Seconds
(without alignments)
1124.814 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactggggccctcc.....ggttcgtgccagaatgtctgc 104

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 1055720 seqs, 742224136 residues

Total number of hits satisfying chosen parameters: 2111440

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEM_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEM_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEM_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	104	100.0	104	US-09-801-371A-1	Sequence 1, Appl1
2	104	100.0	104	US-09-801-371A-5	Sequence 5, Appl1
3	104	100.0	1643	US-10-218-547-3	Sequence 3, Appl1
4	104	100.0	1643	US-10-272-411-4	Sequence 4, Appl1
5	104	100.0	1643	US-10-272-328A-4	Sequence 4, Appl1
6	104	100.0	3634	US-09-824-342B-1	Sequence 1, Appl1
7	104	100.0	3634	US-09-932-300-34	Sequence 34, Appl1
8	104	100.0	81	US-09-801-371A-7	Sequence 7, Appl1
9	50	48.1	50	US-09-801-371A-8	Sequence 8, Appl1
10	43	41.3	43	US-09-801-371A-2	Sequence 2, Appl1
11	43	41.3	43	US-09-801-371A-6	Sequence 6, Appl1
12	42	40.4	418	US-09-796-692-6223	Sequence 6223, Ap
13	42	40.4	418	US-10-040-862-6223	Sequence 6223, Ap
14	33	31.7	51	US-09-801-371A-10	Sequence 10, Appl1
15	27.4	26.3	3617	US-09-874-069-2	Sequence 2, Appl1
16	27.4	26.3	116592	US-09-818-512-3	Sequence 36, Appl1
17	27.2	26.2	122186	US-09-563-728A-36	Sequence 36, Appl1
18	26.8	25.8	2894	US-10-225-567A-669	Sequence 669, Appl1
19	26.8	25.8	3117	US-09-963-766-2	Sequence 2, Appl1

c	20	26.8	25.8	5340	10	US-09-963-766-5	Sequence 5, Appl1
c	21	26.8	25.8	74868	9	US-10-175-523-67	Sequence 67, Appl1
c	22	26.6	25.6	2283	10	US-09-783-590-6687	Sequence 6687, Ap
c	23	26.6	25.6	496	10	US-09-783-590-4240	Sequence 4240, Ap
c	24	26.4	25.4	3347	9	US-10-000-773A-16	Sequence 16, Appl1
c	25	26.4	25.4	4409	9	US-10-216-705-22	Sequence 22, Appl1
c	26	26.4	25.4	6728	9	US-10-060-036-136	Sequence 136, Appl1
c	27	26.4	25.4	6728	9	US-10-171-311-35	Sequence 35, Appl1
c	28	26.4	25.4	6728	9	US-10-149-352-1	Sequence 1, Appl1
c	29	26.4	25.4	6728	10	US-09-854-456-782	Sequence 782, Appl1
c	30	26.4	25.4	6728	10	US-09-880-107-3946	Sequence 3946, Ap
c	31	26.4	25.4	6753	9	US-10-198-846-13252	Sequence 13252, A
c	32	26.4	25.4	6769	9	US-10-198-846-13897	Sequence 13897, A
c	33	26.2	25.2	2650	9	US-10-106-698-2090	Sequence 2090, Ap
c	34	26	25.0	1836	9	US-09-738-626-1225	Sequence 1225, Ap
c	35	26	25.0	26048	9	US-10-091-504-1556	Sequence 1556, Ap
c	36	26	25.0	26048	10	US-09-764-869-1556	Sequence 1556, Ap
c	37	26	25.0	3309400	9	US-09-738-626-1	Sequence 1, Appl1
c	38	25.8	24.8	210	9	US-09-104-750-3	Sequence 10140, A
c	39	25.8	24.8	488	10	US-09-864-761-10140	Sequence 848, Ap
c	40	25.8	24.8	488	10	US-09-783-590-848	Sequence 1031, Ap
c	41	25.8	24.8	603	9	US-10-092-154-1031	Sequence 1031, Ap
c	42	25.8	24.8	603	10	US-09-764-847-1031	Sequence 1031, Ap
c	43	25.8	24.8	717	10	US-09-764-877-3941	Sequence 3941, Ap
c	44	25.8	24.8	3506	9	US-09-104-750-24	Sequence 24, Appl1
c	45	25.8	24.8	4005	10	US-09-349-015-24	Sequence 24, Appl1

ALIGNMENTS

RESULT 1
US-09-801-371A-1
Sequence 1, Application US/09801371A
Patent No. US20020155569A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Jarrons, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801.371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 104
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match 100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAAACTGGGGCTCCAGAACTGAGTGGGCTTGAATCCCTGACATCTG 60
DB 1 GAATCAAACTGGGGCTCCAGAACTGAGTGGGCTTGAATCCCTGACATCTG 60
QY 61 GAATCTGAGACGACGAGGAGCTTTGTTGGCCAGAAATGCTGC 104
DB 61 GAATCTGAGACGACGAGGAGCTTTGTTGGCCAGAAATGCTGC 104

RESULT 2
US-09-801-371A-5/C
Sequence 5, Application US/09801371A
Patent No. US20020155569A1
GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farnat
APPLICANT: Jariou, Navef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801.371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 104
TYPE: DNA
ORGANISM: Homo sapien
US-09-801-371A-5

Query Match 100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGACTGCGGGCCTACAGCTTTGATCCCTGACATCTG 60
DB 104 GAATTCAACTGGGGCCTCCAGACTGCGGGCCTACAGCTTTGATCCCTGACATCTG 45
QY 61 GAATCTGAGACGACGAGGACCTTTGGTCTGGCCAGAAATGCTGC 104
DB 44 GAATCTGAGACGACGAGGACCTTTGGTCTGGCCAGAAATGCTGC 1

RESULT 3
US-10-218-547-3
Sequence 3, Application US/10218547
Publication No. US20030100074A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
FILE REFERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/330,761
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1643
TYPE: DNA
ORGANISM: human
US-10-218-547-3

Query Match 100.0%; Score 104; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGACTGCGGGCCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCCTCCAGACTGCGGGCCTACAGCTTTGATCCCTGACATCTG 1129
QY 61 GAATCTGAGACGACGAGGACCTTTGGTCTGGCCAGAAATGCTGC 104
DB 1130 GAATCTGAGACGACGAGGACCTTTGGTCTGGCCAGAAATGCTGC 1173

RESULT 4
US-10-272-411-4
Sequence 4, Application US/10272411
Publication No. US20030100068A1
GENERAL INFORMATION:

APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1643
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ X01394.1
DATABASE ENTRY DATE: 1995-03-21
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
DATABASE ENTRY DATE: 2002-05-01
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ M35592.1
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
DATABASE ENTRY DATE: 2002-08-01
RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match 100.0%; Score 104; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCCTCCAGACTGCGGGCCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCCTCCAGACTGCGGGCCTACAGCTTTGATCCCTGACATCTG 1129
QY 61 GAATCTGAGACGACGAGGACCTTTGGTCTGGCCAGAAATGCTGC 104
DB 1130 GAATCTGAGACGACGAGGACCTTTGGTCTGGCCAGAAATGCTGC 1173

RESULT 5
US-10-272-328A-4
Sequence 4, Application US/10272328A
Publication No. US20030109444A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0206
CURRENT APPLICATION NUMBER: US/10/272,328A
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1643
TYPE: DNA
ORGANISM: Homo sapiens
US-10-272-328A-4

Query Match 100.0%; Score 104; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTGTATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGGCTCCAGAACTCAGTGGGGCTTGTATCCCTGACATCTG 1129
QY 61 GAATCTGGAGACGAGGAGGAGCTTTGGTCTGGCCAGATGCTGC 104
DB 1130 GAATCTGGAGACGAGGAGGAGCTTTGGTCTGGCCAGATGCTGC 1173

RESULT 6

US-09-824-322B-1
; Sequence 1, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR- α
; FILE REFERENCE: ISPH-0501
; CURRENT APPLICATION NUMBER: US/09/824,322B
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/313,932
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 09/166,186
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; NAME/KEY: exon
; LOCATION: (615)..(981)
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; TITLE: Human lymphotxin and tumor necrosis factor genes: structure, homology and
; TITLE: chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-824-322B-1

Query Match 100.0%; Score 104; DB 9; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1,1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGGCTCCAGAACTCAGTGGGGCTTACAGCTTGTATCCCTGACATCTG 60
DB 2808 GAATTCAACTGGGGGCTCCAGAACTCAGTGGGGCTTGTATCCCTGACATCTG 2867
QY 61 GAATCTGGAGACGAGGAGGAGCTTTGGTCTGGCCAGATGCTGC 104
DB 2868 GAATCTGGAGACGAGGAGGAGCTTTGGTCTGGCCAGATGCTGC 2911

RESULT 7

US-09-932-300-34
; Sequence 34, Application US/09932300
; Publication No. US20030032788A1
; GENERAL INFORMATION:
; APPLICANT: GARVER, Eric
; APPLICANT: TU, Guang-Chou
; APPLICANT: ISRAEL, Yedy
; TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
; FILE REFERENCE: 9855-302
; CURRENT APPLICATION NUMBER: US/09/932,300
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/051,705
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 09/109,663
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-932-300-34

Query Match 100.0%; Score 104; DB 9; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1,1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGGCTCCAGAACTCAGTGGGGCTTGTATCCCTGACATCTG 60
DB 2808 GAATTCAACTGGGGGCTCCAGAACTCAGTGGGGCTTGTATCCCTGACATCTG 2867
QY 61 GAATCTGGAGACGAGGAGGAGCTTTGGTCTGGCCAGATGCTGC 104
DB 2868 GAATCTGGAGACGAGGAGGAGCTTTGGTCTGGCCAGATGCTGC 2911

RESULT 8

US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrons, Nayef
; APPLICANT: Ben-Assoul, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

Query Match 74.0%; Score 77; DB 9; Length 81;
Best Local Similarity 79.2%; Pred. No. 3,1e-18;

```
Matches 61; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATCAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTGTATCCCTGACATCTG 60
DB 5 GAATCAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTGTATCCCTGACATCTG 64
QY 61 GAATCTGAGACACAGG 77
DB 65 GAATCTGAGACACAGG 81

RESULT 9
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jaitous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

Query Match
Best Local Similarity 78.0%; Score 50; DB 9; Length 50;
Matches 39; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTGTATCC 50
DB 1 GAATCAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTGTATCC 50

RESULT 10
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jaitous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2

Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 43;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 47
```

```
DB 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 43

RESULT 11
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jaitous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 43;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 47
DB 43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 1

RESULT 12
US-09-796-692-6223
; Sequence 6223, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE REFERENCE: 2077.001200
; CURRENT FILING DATE: US/09/796, 692
; PRIOR APPLICATION NUMBER: 2001-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/186, 126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/190, 479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200, 545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200, 303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200, 779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200, 999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202, 084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206, 201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218, 950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222, 903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223, 416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223, 378
```

;; PRIOR FILING DATE: 2000-08-07
;; NUMBER OF SEQ ID NOS: 9597
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6223
;; LENGTH: 418
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (1)
;; OTHER INFORMATION: n-A,T,C or G
US-09-796-692-6223

Query Match 40.4%; Score 42; DB 9; Length 418;
Best Local Similarity 90.0%; Pred. No. 1.4e-05;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAATCAAACTGGGGCTCCAGACATCTGAGGCGCTTATGATCC 50
Db 326 GAATCAAACTGGGGCTCCAGACATCTGAGGCGCTTATGATCC 375

RESULT 13
;; Sequence 6223, Application US/10040862
;; Publication No. US20030078396A1
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Algate, Paul A.
;; APPLICANT: Mannion, Jane
;; APPLICANT: Retter, Marc
;; APPLICANT: Corixa Corporation
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
;; FILE REFERENCE: 014058-01352005
;; CURRENT APPLICATION NUMBER: US/10/040,862
;; PRIOR FILING DATE: 2001-11-06
;; PRIOR APPLICATION NUMBER: US 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: US 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: US 60/223,416
;; PRIOR FILING DATE: 2000-08-04
;; PRIOR APPLICATION NUMBER: US 60/223,378
;; PRIOR FILING DATE: 2000-08-07
;; PRIOR APPLICATION NUMBER: US 09/796,692
;; PRIOR FILING DATE: 2001-03-01
;; NUMBER OF SEQ ID NOS: 10467
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6223
;; LENGTH: 418
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (1)
;; OTHER INFORMATION: n-A,T,C or G

US-10-040-862-6223

Query Match 40.4%; Score 42; DB 9; Length 418;
Best Local Similarity 90.0%; Pred. No. 1.4e-05;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAATCAAACTGGGGCTCCAGACATCTGAGGCGCTTATGATCC 50
Db 326 GAATCAAACTGGGGCTCCAGACATCTGAGGCGCTTATGATCC 375

RESULT 14
US-09-801-371a-10

;; Sequence 10, Application US/09801371A
;; Patent No. US20020155569A1
;; GENERAL INFORMATION:
;; APPLICANT: Kaempfer, Raymond
;; APPLICANT: Osman, Farhat
;; APPLICANT: Jarrous, Nayerf
;; APPLICANT: Ben-Asouli, Yitzhak
;; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
;; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
;; CURRENT APPLICATION NUMBER: US/09/801,371A
;; PRIOR FILING DATE: 2001-03-07
;; PRIOR APPLICATION NUMBER: PCT WO 00/14255
;; PRIOR FILING DATE: 1999-09-06
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10
;; LENGTH: 51
;; TYPE: RNA
;; ORGANISM: Oryctolagus cuniculus
US-09-801-371a-10

Query Match 31.7%; Score 33; DB 9; Length 51;
Best Local Similarity 70.7%; Pred. No. 0.017;
Matches 29; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAATCAAACTGGGGCTCCAGACATCTGAGGCGCTTATGATCC 41
Db 1 GCAUUCAAACUGAGGCUCCAGACUCAGGCGCCUUCAG 41

RESULT 15
US-09-874-069-2/c

;; Sequence 2, Application US/09874069
;; Patent No. US20020064826A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Cytokine Receptor-Like Polynucleotides, Polypeptides, and Antl
;; FILE REFERENCE: PTO21P1
;; CURRENT APPLICATION NUMBER: US/09/874,069
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: PCT/US00/32525
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: 60/168,621
;; PRIOR FILING DATE: 1999-12-03
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 3617
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-874-069-2

Query Match 26.3%; Score 27.4; DB 10; Length 3617;
Best Local Similarity 57.6%; Pred. No. 3.3;
Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 20 CAGAACTCACTGGGGCTTATGATCCCTGACATCTGAAATCGAGACGAGGAG 79
Db 969 CTGAATCTGGCTGCGCAATGTCATGTCGCTTACCTGGAACCTGTAGACGTGAAG 910

Wed Jul 2 12:18:21 2003

us-09-801-371a-1.rnpb

Page 6

QY 80 CCTTTGGTCTGGCCAGATGCTGC 104
|| || || || || || || ||
Db 909 GGCTCAGCCTGTCCACATGAAGC 885

Search completed: July 1, 2003, 22:16:13
Job time : 142.252 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 19:55:04 ; Search time 571.871 Seconds

(without alignments)
2188.293 Million cell updates/sec

Title: US-09-801-371a-2

Perfect score: 43

Sequence: 1 tcaactggggcctccagaa.....actggggcctacgcttga 43

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank1:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_ov:*

5: gb_pat:*

6: gb_ph:*

7: gb_pl:*

8: gb_pr:*

9: gb_ro:*

10: gb_sts:*

11: gb_sy:*

12: gb_un:*

13: gb_vl:*

14: em_ba:*

15: em_fun:*

16: em_hum:*

17: em_in:*

18: em_mu:*

19: em_or:*

20: em_ov:*

21: em_pat:*

22: em_ph:*

23: em_pl:*

24: em_ro:*

25: em_sts:*

26: em_un:*

27: em_vl:*

28: em_sy:*

29: em_hum:*

30: em_in:*

31: em_mu:*

32: em_or:*

33: em_ov:*

34: em_pat:*

35: em_ph:*

36: em_pl:*

37: em_ro:*

38: em_sts:*

39: em_un:*

40: em_vl:*

41: em_sy:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	400	11 G13533	G13533 SHGC-11076
2	43	100.0	817	6 A16444	A16444 Xho-PstI fr
3	43	100.0	817	6 E02109	E02109 DNA sequenc
4	43	100.0	1047	9 HSA249755	AJ249755 Homo sapi
5	43	100.0	1275	6 I08430	I08430 Sequence 5
6	43	100.0	1323	6 I07953	I07953 Sequence 6
7	43	100.0	1324	6 E00702	E00702 cDNA encodl
8	43	100.0	1324	6 I03610	I03610 Sequence 2
9	43	100.0	1379	12 SYNTNTRP	M55592 Synthetic h
10	43	100.0	1465	6 I04244	I04244 Sequence 2
11	43	100.0	1560	6 I08863	I08863 Sequence 3
12	43	100.0	1585	6 A37272	A37272 Sequence 12
13	43	100.0	1585	6 I04169	I04169 Sequence 1
14	43	100.0	1585	6 I04198	I04198 Sequence 1
15	43	100.0	1585	6 I08384	I08384 Sequence 5
16	43	100.0	1585	6 I08429	I08429 Sequence 3
17	43	100.0	1585	9 HMTNPA	M10988 Human tumor
18	43	100.0	1606	6 I07541	I07541 Sequence 22
19	43	100.0	1643	6 ARI46199	ARI46199 Sequence
20	43	100.0	1643	9 HSTNFR	X01394 Human mRNA
21	43	100.0	1676	9 BC028148	BC028148 Homo sapi
22	43	100.0	3103	9 HMTNFX	M26331 Human tumor
23	43	100.0	3634	6 ARI00270	ARI00270 Sequence
24	43	100.0	3634	6 ARI49925	ARI49925 Sequence
25	43	100.0	3634	9 HSTNPA	X02910 Human gene
26	43	100.0	4830	9 AY066019	AY066019 Homo sapi
27	43	100.0	7112	6 AX100950	AX100950 Sequence
28	43	100.0	7112	6 AX100965	AX100965 Sequence
29	43	100.0	7112	9 HMTNPA	M16441 Human tumor
30	43	100.0	81800	9 HSTNPA	Z15026 Homo sapien
31	43	100.0	81800	9 HSTNPA	Y14768 Homo sapien
32	43	100.0	100000	9 AP000505	AP000505 Homo sapien
33	43	100.0	135784	9 AL662847	AL662847 Human DNA
34	43	100.0	139399	9 AL662801	AL662801 Human DNA
35	43	100.0	184666	9 DJ201624	AJ129756 Homo sapi
36	43	100.0	212055	2 AP000899	AP000899 Homo sapi
37	38.4	89.3	1455	9 AF019963	AF019963 Papio ham
38	34	79.1	2610	4 HRSTNPA	M64087 Equus cabal
39	30.6	71.2	1671	4 RABTNFM	M12845 Rabbit tumo
40	30.6	71.2	3200	4 RABTNFM	M12846 Rabbit tumo
41	30.6	71.2	6577	4 RABTNFM	M60340 Rabbit lymph
42	27.8	64.7	4349	4 AF011927	AF011927 Bos indic
43	27.8	64.7	4352	4 AF011926	AF011926 Bos tauru
44	27.4	63.7	177917	9 AC025824	AC025824 Homo sapi
45	27.4	63.7	186254	2 AC091544	AC091544 Homo sapi

ALIGNMENTS

RESULT 1

G13533 400 bp DNA linear STS 30-MAR-2000

LOCUS SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.

DEFINITION G13533

ACCESSION G13533

VERSION G13533.1 GI:1129272

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 400)

Oliver, M., and Cox, D.R.

TITLE

Unpublished, Olivier, M., Cox, D.R. (2000)

JOURNAL

COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: oliviereshgc.stanford.edu
Primer A: CACTAGAGATTCAACCTGGGCGC
Primer B: GAGGAGGCGCTAGGTCAC
STS size: 166
PCR Profile:
Initial Incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from M10988 -- Unigene.
Location/Qualifiers

1..400

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="6"

/clone_lib="Human"

STS

primer_bind

complement(356..375)

BASE COUNT

104 a 120 c 87 g 89 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 43; DB 11; Length 400;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCGCTTGA 43

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

BASE COUNT

183 a 268 c 206 g 160 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 43; DB 6; Length 817;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCGCTTGA 43

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

/db_xref="taxon:9606"

BASE COUNT

183 a 268 c 206 g 160 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 43; DB 6; Length 817;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCGCTTGA 43

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

/db_xref="taxon:3847"

BASE COUNT

183 a 268 c 206 g 160 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 43; DB 6; Length 817;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCGCTTGA 43

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

/db_xref="taxon:3847"

BASE COUNT

183 a 268 c 206 g 160 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 43; DB 6; Length 817;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCGCTTGA 43

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1047)
AUTHORS Farhan,A.J., Pravica,V. and Hutchinson,I.V.
TITLE Identification of new rare variant of human TNF-alpha 3' UTR
JOURNAL Unpublished
2 (bases 1 to 1047)
AUTHORS Farhan,A.J.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research Division, Manchester University, Medical School, Stopford Building, Oxford Road, Manchester, M13 9PL, UNITED KINGDOM

FEATURES
source 1..1047
/organism="Homo sapiens"
/db_xref="taxon:9606"
/country="United Arab Emirates"
/note="new rare variant"
1..1047
/gene="TNF-alpha"
1..>1047
/gene="TNF-alpha"
322
variation
/gene="TNF-alpha"
/replace="t"

BASE COUNT 260 a 282 c 221 g 284 t
ORIGIN

Query Match 100.0%; Score 43; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAACTGGGGCCCTCAGAACTCAGTGGGCTACACTTTGA 43
Db 225 TCAACTGGGGCCCTCAGAACTCAGTGGGCTACACTTTGA 267

RESULT 5
108430
LOCUS 108430 1275 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8604606.
ACCESSION 108430
VERSION 108430.1 GI:588860
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CSTEINE-DEPLETED MUTAINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 5 14-AUG-1986;
FEATURES
source 1..1275
Location/Qualifiers
BASE COUNT 297 a 357 c 309 g 312 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1275;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAACTGGGGCCCTCAGAACTCAGTGGGCTACACTTTGA 43
Db 697 TCAACTGGGGCCCTCAGAACTCAGTGGGCTACACTTTGA 739

RESULT 6
107953
LOCUS 107953 1323 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 6 from Patent EP 0168214.
ACCESSION 107953
VERSION 107953.1 GI:589335

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1323)
AUTHORS Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.
TITLE Tumor necrosis factor, methods for its preparation, compositions containing it, DNA encoding it and assay method using such DNA
JOURNAL Patent: EP 0168214-A2 6 15-JAN-1986;
FEATURES
source 1..1323
Location/Qualifiers
BASE COUNT 298 a 387 c 308 g 330 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1323;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAACTGGGGCCCTCAGAACTCAGTGGGCTACACTTTGA 43
Db 754 TCAACTGGGGCCCTCAGAACTCAGTGGGCTACACTTTGA 796

RESULT 7
E00702
LOCUS E00702 1324 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human tumor necrosis factor.
ACCESSION E00702
VERSION E00702.1 GI:2168979
KEYWORDS JP 1986040221-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Barraa,B.A., Debilsudo,B.G., San,H.R. and Guren,E.N.
TITLE TUMOR NECROTIC FACTOR
JOURNAL Patent: JP 1986040221-A 1 26-FEB-1986;
COMMENT
OS homom sapiens
PN JP 1986040221-A/1
PD 26-FEB-1986
PR 05-JUL-1985 JP 1985149075
PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR
03-DEC-1984 US 84 628060, 03-DEC-1984 US 84 677156, PR
03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454 PI BARAA
BUSHIRAN AGAMARU, DEBITSUDDO BANNOOMAN GETSUDERU, PI SAN HII RII,
PI GUREN EBAN NEOUIN
PC A61K35/12,A61K35/02,A61K35/14,A61K37/4,A61K37/04,C07H21/02,
PC C07H21/04,
PC C12N15/00,
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: cell_type=promyelocytes;
CC *source: cell_line=HL-60;
CC *source: clone=lamda42-4, lamda46-4;
FH Key Location/Qualifiers
FT sig_peptide <1..61
FT mat_peptide 62..532
FT <1..535 /product='tumor necrosis factor' FT 3'UTR
FT 536..>1324.
FEATURES
source 1..1324
Location/Qualifiers
BASE COUNT 298 a 387 c 308 g 331 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 43
|||||
DB 755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 797

RESULT 8
LOCUS 103610 1324 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4650674.
ACCESSION 103610
VERSION 103610.1 GI:268632
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Aggarwal, B.B. and Lee, S. He.
TITLE Synergistic cytotoxic composition
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco, CA
FEATURES
source 1..1324
BASE COUNT 298 a 387 c 308 g 331 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1324;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 43
|||||
DB 755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 797

RESULT 9
SYNTPTRP 1379 bp mRNA linear SYN 27-APR-1993
LOCUS Synthetic human tumor necrosis factor mRNA, complete cds.
DEFINITION M35592.1 GI:209485
ACCESSION M35592
VERSION M35592.1 GI:209485
KEYWORDS Altered human leukemic B-cell line Ball-1, CDNA to mRNA, clone
SOURCE PM324-346.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1379)
AUTHORS Nobuhara, M., Kanamori, T., Nagase, Y., Nii, A., Morishita, H.,
Toyama, J., Andoh, S. and Kurimoto, M.
TITLE The expression of human tumor necrosis factor in E. coli
JOURNAL Nucleic Acids Symp. Ser. 17, 131-134 (1986)
MEDLINE 87174864
PUBMED 3031624
FEATURES
source Location/Qualifiers
1..1379
/organism="synthetic construct"
/db_xref="taxon:32630"
178..879
/note="synthetic tumor necrosis factor precursor"
/codon_start=1
/transl_table=1
/protein_id="AAC42098.1"
/db_xref="GI:209486"
/translation="MSTESMIRDVLAELAPKTKGPGSHRCLFLSFLIYAGA
TTLFLHGVGVPQREPPRLSLISPLAQVRSRRPSDKPAHVAVANQAGOL
QMLNRRANALLANGVELRDNLVPSGLIYLSQVLEFKGGCCPSTHYLLTTISRIA
VSQTRKVLNLSIKSPCORETPEGAEAPWETPITLGVFLQLEKSDRUSAEINRDYL
DFAESGVYFIIIAL"

slg_peptide 178..399
mat_peptide 400..876
/note="synthetic tumor necrosis factor signal peptide"
/product="synthetic tumor necrosis factor"

BASE COUNT 318 a 438 c 336 g 287 t
ORIGIN

Query Match 100.0%; Score 43; DB 12; Length 1379;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 43
|||||
DB 1100 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 1142

RESULT 10
LOCUS 104244 1465 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4677197.
ACCESSION 104244
VERSION 104244.1 GI:268725
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1465)
AUTHORS Lin, L.S. and Yamamoto, R.
TITLE Purification method for tumor necrosis factor
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source 1..1465
BASE COUNT 324 a 429 c 363 g 349 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1465;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 43
|||||
DB 887 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 929

RESULT 11
LOCUS 108863 1560 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 8806625.
ACCESSION 108863
VERSION 108863.1 GI:588416
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Mark, D.F., Lin, L.S., Thomson, J.W. and Yamamoto, R.
TITLE ARGININE-DEPLETED HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8806625-A 3 07-SEP-1988;
FEATURES
source Location/Qualifiers
1..1560
/organism="unknown"

BASE COUNT 340 a 473 c 381 g 366 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 43
|||||
DB 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTTACAGCTTTGA 1049

RESULT 12
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9404196.
ACCESSION A37272
VERSION A37272.1 GI:2294369
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Ville, R.G. and Hart, I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
FEATURES
source Location/Qualifiers
1..1585
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 13
LOCUS I04169 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677063.
ACCESSION I04169
VERSION I04169.1 GI:268716
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark, D.F., Wang, A.M., Ladner, M.B., Creasey, A.A., Lin, L.S. and Van
Arsdell, J.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677063-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source 1..1585
/organism="unknown"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 14
LOCUS I04198 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677064.
ACCESSION I04198
VERSION I04198.1 GI:268719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark, D.F., Wang, A.M., Ladner, M.B., Creasey, A.A., Van Arsdell, J.N.
and Lin, L.S.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677064-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source 1..1585
/organism="unknown"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 15
LOCUS I08384 1585 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8602381.
ACCESSION I08384
VERSION I08384.1 GI:588904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark, D.F., Wang, A.M., Ladner, M.B., Creasey, A.A., Lin, L.S. and Van
Arsdell, J.N.
TITLE HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;
Location/Qualifiers
1..1585
/organism="unknown"
BASE COUNT 352 a 473 c 389 g 371 t
ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

Search completed: July 1, 2003, 21:27:27
Job time : 572.871 secs

THIS PAGE BLANK (USPTO)

[illegible]

PT cis-acting nucleotide sequence controlled by phosphorylation of the
 PT alpha-subunit of eukaryotic initiation factor 2
 XX
 PS Claim 5, Page 15; 75pp; English.
 CC The specification describes a cis-acting nucleotide sequence which is
 CC capable of removing introns from a precursor transcript encoded by a
 CC gene which harbours at least one cis-acting nucleotide sequence. This
 CC removal is effected during the production of mRNA of the gene, and
 CC depends on activation of a trans-acting factor which is an RNA-activated
 CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
 CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
 CC sequence, derived from the 3' untranslated region (3'UTR) of the human
 CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
 CC splicing of precursor transcripts encoded by that gene sensitive to the
 CC level of RNA-activated protein kinase (PKR) activity. The sequence can
 CC be used to transform host cells to regulate gene expression at the mRNA
 CC splicing level, for gene therapy, and to produce a recombinant
 CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
 CC protein) or industrially or agriculturally applicable protein. The
 CC present sequence represents a cis-acting nucleotide sequence of the
 CC invention.
 CC
 SO Sequence 43 BP; 10 A; 13 C; 11 G; 9 T; 0 other;
 Query Match 100.0%; Score 43; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TCMAACTGGGGCCTCAGAACTCAGTGGGGCCTACAGCTTGA 43
 DB 1 TCMAACTGGGGCCTCAGAACTCAGTGGGGCCTACAGCTTGA 43
 RESULT 2
 AA299815
 ID AA299815 standard; RNA; 50 BP.
 AC AA299815;
 XX
 DT 12-JUL-2000 (first entry)
 DE Sequence of the stem loop of tumour necrosis factor-alpha gene.
 XX
 KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
 KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
 KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200014255-A1.
 PD 16-MAR-2000.
 XX
 PF 06-SEP-1999; 99WO-IL00483.
 XX
 PR 07-SEP-1998; 98IL-0126112.
 PR 26-OCT-1998; 98IL-0126757.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
 XX
 DR WPI: 2000-257000/22.
 XX
 PT Regulation of gene expression by mRNA splicing is carried out using a
 PT cis-acting nucleotide sequence controlled by phosphorylation of the
 PT alpha-subunit of eukaryotic initiation factor 2
 XX
 PS Example 7; Fig 5B; 75pp; English.
 CC The specification describes a cis-acting nucleotide sequence which is
 CC capable of removing introns from a precursor transcript encoded by a

CC gene which harbours at least one cis-acting nucleotide sequence. This
 CC removal is effected during the production of mRNA of the gene, and
 CC depends on activation of a trans-acting factor which is an RNA-activated
 CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
 CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
 CC sequence, derived from the 3' untranslated region (3'UTR) of the human
 CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
 CC splicing of precursor transcripts encoded by that gene sensitive to the
 CC level of RNA-activated protein kinase (PKR) activity. The sequence can
 CC be used to transform host cells to regulate gene expression at the mRNA
 CC splicing level, for gene therapy, and to produce a recombinant
 CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
 CC protein) or industrially or agriculturally applicable protein. The
 CC present sequence represents a fragment of the 3'UTR of human TNF-alpha.
 CC
 SO Sequence 50 BP; 12 A; 15 C; 12 G; 11 U; 0 other;
 Query Match 100.0%; Score 43; DB 21; Length 50;
 Best Local Similarity 79.1%; Pred. No. 1.6e-07;
 Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TCMAACTGGGGCCTCAGAACTCAGTGGGGCCTACAGCTTGA 43
 DB 5 UCMAACUGGGCCUCCAGAACUCACUGGGCCUACAGCUUUA 47
 RESULT 3
 AA299816
 ID AA299816 standard; RNA; 104 BP.
 AC AA299816;
 XX
 DT 12-JUL-2000 (first entry)
 DE Cis-acting nucleotide sequence derived from human TNF-alpha.
 XX
 KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
 KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
 KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200014255-A1.
 PD 16-MAR-2000.
 XX
 PF 06-SEP-1999; 99WO-IL00483.
 XX
 PR 07-SEP-1998; 98IL-0126112.
 PR 26-OCT-1998; 98IL-0126757.
 XX
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
 XX
 DR WPI: 2000-257000/22.
 XX
 PT Regulation of gene expression by mRNA splicing is carried out using a
 PT cis-acting nucleotide sequence controlled by phosphorylation of the
 PT alpha-subunit of eukaryotic initiation factor 2
 XX
 PS Claim 4; Page 15; 75pp; English.
 CC The specification describes a cis-acting nucleotide sequence which is
 CC capable of removing introns from a precursor transcript encoded by a
 CC gene which harbours at least one cis-acting nucleotide sequence. This
 CC removal is effected during the production of mRNA of the gene, and
 CC depends on activation of a trans-acting factor which is an RNA-activated
 CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
 CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
 CC sequence, derived from the 3' untranslated region (3'UTR) of the human
 CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
 CC splicing of precursor transcripts encoded by that gene sensitive to the

CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention.

XX
SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
Db 5 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 47

RESULT 4
AAZ20979
ID AAZ20979 standard; DNA; 787 BP.
XX
AC AAZ20979;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human TNFalpha 3'UTR.
XX
KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus;
KW diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
PN MO9943840-A1.
XX
PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99MO-US00637.
XX
PR 27-FEB-1998; 98US-0076316.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Talarke RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX
PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
PS promoter and an apoptosis-inducing Granzyme B polynucleotide
XX
XX Example 1; Page 60-61; 71pp; English.

CC This sequence represents a human TNFalpha (tumour necrosis factor alpha)
CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984)
CC were constructed comprising at least one TNFalpha promoter enhancer
CC region (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA
CC encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a
CC TNFalpha 3'UTR sequence. TNFalpha is one of a number of
CC cytokines produced by inflammatory cells. Upregulation and/or
CC dysregulation of cytokines in inflamed tissue may be directly or
CC indirectly responsible for exacerbation of chronic inflammatory
CC diseases. Introduction of the chimeric nucleotide to activated
CC inflammatory cells causes them to undergo apoptosis. Pharmaceutical
CC compositions of the chimeric nucleotide may be useful for treating
CC inflammatory disorders such as multiple sclerosis, Crohn's disease,
CC ulcerative colitis, psoriasis, graft versus host disease, lupus
CC erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing
CC spondylitis, and in particular, rheumatoid arthritis. The use of such
CC chimeric nucleotides offers simpler and cheaper long-term relief, in
CC comparison with existing conventional pharmaceutical and invasive surgery

CC methods.

XX
SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;

Query Match 100.0%; Score 43; DB 20; Length 787;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
Db 226 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 268

RESULT 5
AAN70075
ID AAN70075 standard; DNA; 815 BP.
XX
AC AAN70075;
XX
DT 20-JAN-1991 (first entry)
XX
DE Human anti-tumor polypeptide Xho-PstI fragment.
XX
KW Anti-tumor; cancer; cytotoxic; ss.
XX
OS Homo sapiens.
XX
PN EP247906-A.
XX
PD 02-DEC-1987.
XX
PF 04-FEB-1987; 87EP-0400261.
XX
PR 17-JUL-1986; 86JP-0169522.
XX
PR 04-FEB-1986; 86JP-0021302.
XX
PA (MIZU/) MIZUNO D.
XX
PI Mizuno D;
XX
PI Soma GI;
XX
DR WPI; 1987-336540/48.
XX
PT Anti-tumor polypeptides - prepared using recombinant DNA prepared
PS from genomic DNA of human acute leukemia cell THP-1.
XX
PS Disclosure; Fig 7; 63pp; English.

CC The sequence is an Xho-PstI fragment of an anti-tumor protein.
CC The polypeptide is cytotoxic to human tumor cells but not to normal
CC cells. They are also cytotoxic to primary cell cultures obtained
CC from metastasis lesions of patients suffering from striated muscle
CC tumors. They are also resistant to all chemotherapeutic agents.
CC See also AAN70073-74, AAN70077-78 and AAP95592.
XX
XX

XX
SQ Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 other;

Query Match 100.0%; Score 43; DB 8; Length 815;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 43
Db 716 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTACAGCTTTGA 758

RESULT 6
AAQ04340
ID AAQ04340 standard; DNA; 817 BP.
XX
AC AAQ04340;
XX
DT 21-SEP-1990 (first entry)

```

XX THP-1.
DE Acute leukemia cell; THP-1; anti-tumour agent; ss.
XX
XX Homo sapiens.
XX JP02088598-A.
XX
XX 28-MAY-1990.
XX
XX 22-SEP-1988; 88JP-0239154.
XX
XX 22-SEP-1988; 88JP-0239154.
XX
XX (SOMA/) SOMA G.
XX
XX WPI; 1990-143138/19.
XX
XX Intrinsic TNF prodn. derivation agents - contain primer and trigger,
XX at least one of which has TNF activity.
XX
XX Disclosure; ; P; Japanese.
XX
XX Used in the prodn. of TNF prodn. agents.
XX
XX Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 other;
XX
Query Match 100.0%; Score 43; DB 11; Length 817;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 43
DB 716 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 758
RESULT 7
AAN91035
ID AAN91035 standard; DNA; 818 BP.
XX
XX AAN91035;
XX
XX 11-MAR-1990 (first entry)
XX
XX XhoI - PstI section of gene for anti-cancer peptide.
XX
XX Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX
XX THP-1 cells.
XX
XX JP01095784-A.
XX
XX 13-APR-1989.
XX
XX 06-OCT-1987; 87JP-0252174.
XX
XX 06-OCT-1987; 87JP-0252174.
XX
XX (SENG/) SEN G.
XX
XX WPI; 1989-154899/21.
XX
XX Novel DNA, plasmid and polypeptide(s)
XX - useful as anticarcinogenic agents
XX
XX Fig 3; ; 17pp; Japanese.
XX
XX Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA
XX from THP-1 cells.
XX
XX Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 other;
XX

```

```

Query Match 100.0%; Score 43; DB 10; Length 818;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 43
DB 717 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 759
RESULT 8
AAN70072
ID AAN70072 standard; DNA; 1200 BP.
XX
XX AAN70072;
XX
XX 20-JAN-1991 (first entry)
XX
XX Human anti-tumor polypeptide.
XX
XX Anti-tumor; cancer; cytotoxic; ss.
XX
XX Homo sapiens.
XX
XX EP247906-A.
XX
XX 02-DEC-1987.
XX
XX 04-FEB-1987; 87EP-0400261.
XX
XX 17-JUL-1986; 86JP-0169522.
XX
XX 04-FEB-1986; 86JP-0021302.
XX
XX (MIZU/) MIZUNO D.
XX
XX Mizuno D;
XX
XX Soma GI;
XX
XX WPI; 1987-336540/48.
XX
XX Anti-tumor polypeptides - prepared using recombinant DNA prepared
XX from genomic DNA of human acute leukemia cell THP-1.
XX
XX Disclosure; Fig 4; 63pp; English.
XX
XX The polypeptide is cytotoxic to human tumor cells but not to normal
XX cells. They are also cytotoxic to primary cell cultures obtained
XX from metastasis lesions of patients suffering from striated muscle
XX tumors. They are also resistant to all chemotherapeutic agents.
XX
XX See also AAN70073-75, AAN70077-78 and AAN95592.
XX
XX Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;
XX
Query Match 100.0%; Score 43; DB 8; Length 1200;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 43
DB 1099 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 1141
RESULT 9
AAN90969
ID AAN90969 standard; DNA; 1200 BP.
XX
XX AAN90969;
XX
XX 11-MAR-1990 (first entry)
XX
XX Part of gene for anti-cancer peptide.
XX
XX Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX

```


OS THP-1 cells.
 XX
 PN JP01095784-A.
 XX
 PD 13-APR-1989.
 XX
 PF 06-OCT-1987; 87JP-0252174.
 XX
 PR 06-OCT-1987; 87JP-0252174.
 XX
 PA (SENG) SEN G.
 XX
 DR WPI: 1989-154899/21.
 XX
 PT Novel DNA, plasmid and polypeptide(s)
 XX - useful as anticarcinogenic agents
 XX
 PS Fig 2; 17pp; Japanese.
 XX
 CC Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1
 CC cells.
 CC
 SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;
 Query Match 100.0%; Score 43; DB 10; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTGA 43
 DB 1099 TCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTGA 1141
 RESULT 10
 ID AAN60558 standard; DNA; 1275 BP.
 XX
 AC AAN60558;
 XX
 DT 28-JUL-1991 (first entry)
 XX
 DE Sequence encoding mature human tumour necrosis factor (hTNF) mutain
 DE Ser 69 in PAW731.
 XX
 KM Antitumour; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..474
 FT /*tag- a
 XX
 PN MO8604606-A.
 XX
 PD 14-AUG-1986.
 XX
 PF 03-FEB-1986; 86MO-US00236.
 XX
 PR 07-FEB-1985; 85US-0698939.
 PR 15-OCT-1982; 82US-0435154.
 PR 15-APR-1983; 83US-0486162.
 PR 20-DEC-1983; 83US-0564224.
 PR 15-OCT-1984; 84US-0661026.
 PR 07-FEB-1985; 85US-0695934.
 XX
 PA (CETU) CETUS CORP.
 XX
 PI Mark DF, Lin LS, Lu SD, Wang AM;
 XX
 DR WPI: 1986-225458/34.
 DR P-PSDB; AAP60656.
 XX
 PT New synthetic mutains of human tumour necrosis factor protein -

PT are obtd. by direct mutagenesis and retain antitumour activity
 XX
 PS Disclosure; Fig 3a; 47pp; English.
 XX
 CC The sequence encoding TNF produced by the promyelocytic leukemia
 CC cell line (HL-60, ATCC no. CCL240) has been cloned and expressed in
 CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
 CC the TNF sequence appears to be involved in disulphide linkages. The
 CC patentors claim a novel synthetic mutain of a biologically active
 CC hTNF protein, having at least one cysteine residue free from a
 CC disulphide link and non-essential to the activity and having at
 CC least one of the cysteine residues deleted or replaced by another AA.
 CC Plasmid PAW731 (Ser 69) is claimed.
 CC
 SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;
 Query Match 100.0%; Score 43; DB 7; Length 1275;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTGA 43
 DB 697 TCAAACTGGGGCCTCCAGAACTCAGTGGGGCTTGA 739
 RESULT 11
 ID AAN60363 standard; DNA; 1323 BP.
 XX
 AC AAN60363;
 XX
 DT 19-JUN-1991 (first entry)
 XX
 DE Sequence encoding human tumour necrosis factor.
 XX
 KM hTNF; tumour; cancer; interferon; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..534
 FT /*tag- a
 FT sig-peptide 1..60
 FT /*tag- b
 FT mat-peptide 61..534
 FT /*tag- c
 XX
 PN EP168214-A.
 XX
 PD 15-JAN-1986.
 XX
 PF 03-JUL-1985; 85EP-0304758.
 XX
 PR 03-DEC-1984; 84US-0677454.
 PR 05-JUL-1984; 84US-0627959.
 PR 05-JUL-1984; 84US-0628059.
 PR 05-JUL-1984; 84US-0628060.
 PR 03-DEC-1984; 84US-0677156.
 PR 03-DEC-1984; 84US-0677257.
 PR 25-JUL-1984; 84US-0627969.
 PR 03-DEC-1984; 84US-0677267.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;
 XX
 DR WPI: 1986-015483/03.
 DR P-PSDB; AAP60417.
 XX
 PT Pure tumour necrosis factor and mutant forms - new DNA coding
 XX sequences and transformed cells.

PS Claim 20; Fig 10; 90pp; English.

XX Sequence encodes the pure human tumour necrosis factor, mutants of

CC which are covered by the claims. TNF and mutants are useful in

CC treating tumours, especially in tandem with interferon. The

CC encoding sequence may be used to create plasmid pTRAPXPTNF, allowing

CC transformation of an E. coli host for the expression of TNF.

XX

SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;

Query Match 100.0%; Score 43; DB 7; Length 1323;

Best Local Similarity 100.0%; Pred. No. 2,7e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGA 43

DB 754 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGA 796

RESULT 12

ID AAF21085 standard; DNA; 1324 BP.

XX AAF21085;

AC AAF21085;

XX 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2652.

XX

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;

KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiallergic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

XX

PD 26-OCT-2000.

XX

PF 24-MAR-2000; 2000WO-US08020.

XX

PR 06-APR-1999; 99US-0127958.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI: 2000-679539/66.

XX

XX Low adenosine (A) content antisense oligonucleotides which do not

PT trigger adenosine receptors during metabolism, useful e.g. for treating

PT cancers and respiratory obstructions -

XX

PS Disclosure: Page 887; 1592pp; English.

XX

XX The present invention describes low adenosine (A) content antisense

CC oligonucleotides and compositions (I) comprising them. In the antisense

CC oligonucleotides the A is replaced by a 'Universal' or alternative base.

CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.

CC The antisense oligonucleotides and (I) can be used to down-regulate the

CC expression and or activity of target polypeptides associated with

CC lung/respiratory disorders and malignancies, such as stimulating and

CC activating peptide factors and transmitters, transcription factors,

CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC chemokines, endogenously produced specific and non-specific enzymes,

CC binding proteins, adhesion molecules and their receptors, cytokine and

CC chemokine receptors, adenosine receptors, bradykinin receptors, central

CC nervous system (CNS) and peripheral nervous and non-nervous system

CC receptors, CNS and peripheral nervous and non-nervous system peptide

CC transmitters, defensins, growth factors, vasoactive peptides and

CC receptors, binding proteins and malignancy associated proteins. The

CC antisense oligonucleotides may be used in this way to treat disorders

CC including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)

CC and/or surfactant hypoproduction which are associated with a disease or

CC condition selected from pulmonary vasoconstriction, inflammation,

CC allergies, asthma, impeded respiration, respiratory distress syndrome

CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),

CC pulmonary transplantation rejection, pulmonary infections, bronchitis,

CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide

CC fragments and antisense oligonucleotides used in the exemplification of

CC the present invention.

XX

SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 1324;

Best Local Similarity 100.0%; Pred. No. 2,7e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGA 43

DB 755 TCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGA 797

RESULT 13

ID AAA34963 standard; DNA; 1324 BP.

XX AAA34963;

AC AAA34963;

XX

XX 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.

XX

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiallergic; cytostatic; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX

OS Homo sapiens.

XX

PN WO200009525-A2.

XX

PD 24-FEB-2000.

XX

PF 03-AUG-1999; 99WO-US17712.

XX

PR 03-AUG-1998; 98US-0095212.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA

XX

PI Nyce JW;

XX

DR WPI: 2000-205971/18.

XX

XX New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers -

XX

PS Disclosure: Page 814-815; 1343pp; English.

CC E.coli (see AAM60557). Neither of the cysteine residues (69 and 101) in
CC the TNF sequence appears to be involved in disulphide linkages. The
CC patentors claim a novel synthetic mutcin of a biologically active
CC hTNF protein, having at least one cysteine residue free from a
CC disulphide link and non-essential to the activity and having at
CC least one of the cysteine residues deleted or replaced by another AA.
CC Plasmid pMW731 (Ser 69) is claimed.
XX

SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;

Query Match 100.0%; Score 43; DB 7; Length 1585;

Best Local Similarity 100.0%; Pred. No. 2.8e-07;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGGCTCCAGAACTCAGACGCGGCTACAGCTTTGA 43

DB 1007 TCAAACTGGGGGCTCCAGAACTCAGACGCGGCTACAGCTTTGA 1049

Search completed: July 1, 2003, 20:54:33
Job time : 100.163 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:41:41 ; Search time 765.81 seconds
(without alignments)
909.372 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43
Sequence: 1 tcaaacctggggcctccagaa.....actggggcctacagcttga 43

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	248	14	T29839 EST97164 Hu
2	43	100.0	722	14	BQ007008 UI-H-E11
3	43	100.0	1014	9	AL543083 AL543083
4	35.2	81.9	581	9	AT242177 qh81g08.x
5	33.6	78.1	564	9	AA696697 z178f12.s
6	28	65.1	561	12	BG232086 natf32e06

Result	Score	Query Match	Length	DB ID	Description
1	43	100.0	248	14	T29839 EST97164 Hu
2	43	100.0	722	14	BQ007008 UI-H-E11
3	43	100.0	1014	9	AL543083 AL543083
4	35.2	81.9	581	9	AT242177 qh81g08.x
5	33.6	78.1	564	9	AA696697 z178f12.s
6	28	65.1	561	12	BG232086 natf32e06

ALIGNMENTS

RESULT 1
T29839
LOCUS
DEFINITION
T29839
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 248)
Adams,M.D., Keriavase,A.R., Fleischmann,R.D., Fulmer,R.A., Bult
,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Chin,M.-W., Clayton,R.A.,
Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.M., Glodok,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,P.S., Kelley,J.M.,
Klimke,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shifley,R.,
Small,K.V., Spriggs,T.A., Utecherback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,
DiMeo,D., Feng,P., Ferris,A., Fischer,C., Hastings,G.A., He,W.-W.,
Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L.,
Kunsch,C., Li,H., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei
,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

TITLE
Initial Assessment of Human Gene Diversity and Expression Patterns
JOURNAL
Based Upon 83 Million Basepairs of cDNA Sequence
MEDLINE
Nature 377, 3-174 (1995)
COMMENT
96026280
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M3 Reverse.

FEATURES
source
1.248
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="ATCC (lnost):107667"
/db_xref="taxon:9606"
/clone.lib="Human Testis"
/note="Organ: testis"

BASE COUNT
63 a 65 c 60 g 57 t 3 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 43; DB 14; Length 248;
Pred. No. 8.6e-06;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TCMAACTGGGCGCTCCAGACTCAGTGGGCGCTTGA 43
|||||
62 TCMAACTGGGCGCTCCAGACTCAGTGGGCGCTTGA 104
|||||

RESULT 2
LOCUS BQ007008 722 bp mRNA linear EST 26-MAR-2002
DEFINITION UI-H-EII-a2b-j-22-0-UI.s1 NCI CGAP_EII Homo sapiens cDNA clone
IMAGE:5846517 3', mRNA sequence.
ACCESSION BQ007008
VERSION BQ007008.1 GI:19731908
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 722)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgrabs-remail.nih.gov

JOURNAL
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/ILIN at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAA)nSimple_repeat
Seq primer: M3 FORWARD
POLYA=yes.

FEATURES
source
1.722
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="IMAGE:5846517"
/clone.lib="NCI CGAP_EII"
/tissue.type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT7n3-Pac (Pharmacia)

with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7n3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(GT)₁₈ tail. The sequence tag for this library is
ACACTGCAC.
TAG LIB-UI-H-EII
TAG TISSUE=chondrosarcoma
TAG_SEQ=ACACTGCAC

BASE COUNT
204 a 162 c 164 g 190 t 2 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 43; DB 14; Length 722;
Pred. No. 1.1e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TCMAACTGGGCGCTCCAGACTCAGTGGGCGCTTGA 43
|||||
591 TCMAACTGGGCGCTCCAGACTCAGTGGGCGCTTGA 549
|||||

RESULT 3
LOCUS AL543083 1014 bp mRNA linear EST 16-FEB-2001
DEFINITION AL543083 LVI_NFL006.PL2 Homo sapiens cDNA clone CSOD1002YE03 3
prime, mRNA sequence.
ACCESSION AL543083
VERSION AL543083.1 GI:12875561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1014)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1.1014
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1002YE03"
/clone.lib="LVI_NFL006.PL2"
/tissue.type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifestech.com URL :
<http://fulllength.invitrogen.com>

BASE COUNT
265 a 232 c 281 g 234 t 2 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 1014;
Pred. No. 1.2e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TCMAACTGGGCGCTCCAGACTCAGTGGGCGCTTGA 43
|||||

Db	548	TCAAACTGGGCGCTCCAGAACTCAGTGGGCGCTACAGCTTTGA	506
RESULT 4			
LOCUS	AI242177/c		
DEFINITION	AI242177	581 bp mRNA linear EST 01-DEC-1998	
ACCESSION	AI242177	gbl1908.x1 Soares fetal_liver_spleen_JNFLS.S1 Homo sapiens CDNA	
VERSION	AI242177	clone IMAGE:1851134 3' similar to gb:M10988 TUMOR NECROSIS FACTOR	
KEYWORDS	EST.	PRECUSOR (HUMAN); mRNA sequence.	
SOURCE	AI242177.1 GI:3837574		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
FEATURES	Tumor Gene Index		
SOURCE	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	Insert Length: 1280 Std Error: 0.00		
	Seq primer: -400P from Gdbco		
	High quality sequence stop: 463.		
	Location/Qualifiers		
	1. 581		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1851134"		
	/clone_id="Soares.fetal_liver_spleen_JNFLS.S1"		
	/sex="male"		
	/dev_stage="20 week-post conception fetus"		
	/lab_host="DH10B (ampicillin resistant)"		
	/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)		
	with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;		
	This is a subtracted version of the original Soares fetal		
	liver spleen JNFLS library. 1st strand cDNA was primed		
	with a Pac I - oligo(dT) primer [5',		
	AACGGAAGAATTAATTAAAGATCTTTTCTTTTCTTTTCTTTT 3'],		
	double-stranded cDNA was ligated to Eco RI adaptors		
	(Pharmacia), digested with Pac I and cloned into the Pac I		
	and Eco RI sites of the modified pT7T3 vector. Library		
	went through one round of normalization. Library		
	constructed by Bento Soares and M.Fatima Bonaldo."		
BASE COUNT	179 a 130 c 135 g 137 t		
ORIGIN			
Query Match	81.9%; Score 35.2; DB 9; Length 581;		
Best Local Similarity	92.5%; Pred. No. 0.0079;		
Matches	37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
OY	4 AACTGGGGCGCTCCAGAACTCAGTGGGCGCTACAGCTTTGA 43		
Db	574 AAACGTGGCGCTCCAGAACTCAGTGGGCGCTACAGCTTTGA 535		
RESULT 5			
LOCUS	AA699697/c	564 bp mRNA linear EST 19-DEC-1997	
DEFINITION	AA699697	z178f12.s1 Soares fetal_liver_spleen_JNFLS.S1 Homo sapiens CDNA	
ACCESSION	AA699697	clone IMAGE:446927 3' similar to gb:M10988 TUMOR NECROSIS FACTOR	
VERSION	AA699697.1 GI:2703844	PRECUSOR (HUMAN); mRNA sequence.	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 564)	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.				
WashU-NCI human EST project				
Unpublished (1997)				
Contact: Wilson RK				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
Tel: 314 286 1800				
Fax: 314 286 1810				
Email: estewatson.wustl.edu				
This clone is available royalty-free through LINT; contact the				
IMAGE Consortium (info@image.llnl.gov) for further information.				
Seq primer: -40ml3 fwd. ET from Amersham				
High quality sequence stop: 397.				
Location/Qualifiers				
1..564				
/organism="Homo sapiens"				
/db_xref="GDB:1351184"				
/db_xref="taxon:9606"				
/clone="IMAGE:446927"				
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"				
/sex="Male"				
/dev_stage="20 week-post conception fetus"				
/lab_host="DH10B (ampicillin resistant)"				
/note="Organ: Liver and Spleen; Vector: pTZ19 (Pharmacia)				
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI;				
This is a subcloned version of the original Soares fetal				
liver spleen INFLS library. 1st strand cDNA was primed				
with a Pac I - Oligo(dT) primer [5']				
AACGGAAGAATTATTAAGATCTTTTTTTTTTTTTTTT 3'],				
double-stranded cDNA was ligated to Eco RI adaptors				
(Pharmacia), digested with Pac I and cloned into the Pac I				
and Eco RI sites of the modified pTZ19 vector. Library				
went through one round of normalization. Library				
constructed by Bento Soares and M.Fatima Bonaldo."				
BASE COUNT	176 a	123 c	138 g	127 t
ORIGIN				
Query Match	78.18;	Score 33.6;	DB 9;	Length 564;
Best Local Similarity	90.08;	Pred. No. 0.031;		
Matches	36;	Conservative 0;	Mismatches 4;	Indels 0;
Gaps	0;			
Oy	1	TCAACTGGGCTCCAGAACTCACTGAGGGCTACAGCTT	40	
Db	561	TCAACTGGGCTCCAGAACTCACTGAGGGCTACAGCTT	522	
RESULT 6				
BG232086/c				
LOCUS	BG232086	561 bp	mRNA	linear
DEFINITION	na332086.x1 Soares_NPBMC Homo sapiens CDNA clone IMAGE:4142698 3',			
ACCESSION	BG232086			
VERSION	BG232086.1	GI:12727241		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Estuaries; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
COMMENT	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgaaps-remail.nih.gov			
	Tissue Procurement: M. Bento Soares, Ph.D.			
	CDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima			
	Bonaldo, Ph.D.			

RESULT 9
N26123
LOCUS
DEFINITION
N26123
594 bp mRNA linear EST 29-DEC-1995
YX30H08.S1 Soares melanocyte 2NBM Homo sapiens cDNA clone
IMAGE:265055 3' similar to gb|U87890|HWDALCE124 Human carcinoma
cell-derived Alu RNA transcript, (rRNA); gb:U4008_rnal LYSOZYME C
PRECUSOR (HUMAN); contains Alu repetitive element; mRNA sequence.
N26123
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucab, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Ridkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,
R., Williamson, A., Wohlmann, P. and Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence stops: 427
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 427.
Location/Qualifiers
1..594
/organism="Homo sapiens"
/db_xref="GDB:3878697"
/db_xref="taxon:9606"
/clone="IMAGE:265055"
/clone_lib="Soares melanocyte 2NBM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT733 (pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5,
TGTTCACATCTGAGTGGAGCGCGCAGCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

BASE COUNT 158 a 135 c 110 g 186 t 5 others
ORIGIN
Query Match 55.8%; Score 24; DB 14; Length 594;
Best Local Similarity 75.0%; Pred. NO. 1.1e+02;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 4 AACTGGGGCTCCAGACTCAGTGGGCTCAGCTTTGA 43
|||||
DB 411 ACCTCAGGCTCCCAAACTGCTGGGATTCAGGTGCA 450
|||||

RESULT 10
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

BF737938 163 bp mRNA linear EST 10-JAN-2001
CM2-KT0031-141200-628-c08 KT0031 Homo sapiens cDNA, mRNA sequence.
BF737938 BF737938.1 GI:12064614
EST..
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
SOURCE

Das Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-KT0031-
141200-628-c08&tl3=2000-12-14&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 4
High quality sequence stop: 77.
Location/Qualifiers
1..163
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KT0031"
/dev_stage="Adult"
/note="Organ: bladder_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 34 a 50 c 35 g 44 t
ORIGIN
Query Match 55.3%; Score 23.8; DB 12; Length 163;
Best Local Similarity 80.0%; Pred. NO. 95;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 5 ACTGGGGCTCCAGACTCAGTGGGCTTACAGCT 39
|||||
DB 1 ACTGGTCCATCATGCTCAGTGGGCTCCAGCT 35
|||||

RESULT 11
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

BF855413 172 bp mRNA linear EST 16-JAN-2001
RC4-FN0203-121100-011-b01 FN0203 Homo sapiens cDNA, mRNA sequence.
BF855413 BF855413.1 GI:12243157
EST..
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

THIS PAGE BLANK (USPTO)

ANTI-SENSE: NO
ORIGINAL SOURCE: TNF CDNA HSTNFR (EMBL Accession
INDIVIDUAL ISOLATE: #X01394)
INDIVIDUAL ISOLATE: #X01394)
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 153..851
US-08-880-342-36

Query Match 100.0%; Score 43; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGACTCAGTGGGCTTGA 43
|||||
Db 1074 TCAAACTGGGGCCTCCAGACTCAGTGGGCTTGA 1116

RESULT 2
US-09-505-250-4
Sequence 4, Application US/09505250A
Patent No. 6329148
GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 1643
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (153)..(854)
US-09-505-250-4

Query Match 100.0%; Score 43; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGACTCAGTGGGCTTGA 43
|||||
Db 1074 TCAAACTGGGGCCTCCAGACTCAGTGGGCTTGA 1116

RESULT 3
US-09-166-186-1
Sequence 1, Application US/09166186A
Patent No. 6080580
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- α EXPRESSION
FILE REFERENCE: ISPH-0322
CURRENT APPLICATION NUMBER: US/09/166,186A
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 250
SEQ ID NO 1
LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
FEATURE:
NAME/KEY: exon

LOCATION: (615)..(981)
FEATURE:
NAME/KEY: Intron
LOCATION: (982)..(1588)
FEATURE:
NAME/KEY: exon
LOCATION: (1589)..(1634)
FEATURE:
NAME/KEY: Intron
LOCATION: (1635)..(1821)
FEATURE:
NAME/KEY: exon
LOCATION: (1822)..(1869)
FEATURE:
NAME/KEY: Intron
LOCATION: (1870)..(2070)
FEATURE:
NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
TITLE: Homology and chromosomal localization
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

Query Match 100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGACTCAGTGGGCTTGA 43
|||||
Db 2812 TCAAACTGGGGCCTCCAGACTCAGTGGGCTTGA 2854

RESULT 4
US-09-313-932-1
Sequence 1, Application US/09313932A
Patent No. 6228642
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- α EXPRESSION
FILE REFERENCE: ISPH-0356
CURRENT APPLICATION NUMBER: US/09/313,932A
CURRENT FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 501
SEQ ID NO 1
LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
FEATURE:
NAME/KEY: exon
LOCATION: (615)..(981)

FEATURE: intron
NAME/KEY: (982)..(1588)
LOCATION: (982)..(1588)
FEATURE:
NAME/KEY: exon
LOCATION: (1589)..(1634)
FEATURE:
NAME/KEY: intron
LOCATION: (1635)..(1821)
FEATURE:
NAME/KEY: exon
LOCATION: (1822)..(1869)
FEATURE:
NAME/KEY: intron
LOCATION: (1870)..(2070)
FEATURE:
NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes:
TITLE: structure, homology and chromosomal localization
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match 100.0%; Score 43; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 43
Db 2812 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 2854

RESULT 5
US-09-109-663-34
Sequence 34, Application us/09109663
Patent No. 6277981
GENERAL INFORMATION:
APPLICANT: Tu, Guang-Chou
APPLICANT: Israel, Yedy
TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
FILE REFERENCE: 9855-3U1
CURRENT APPLICATION NUMBER: US/09/109, 663
CURRENT FILING DATE: 1998-07-03
EARLIER APPLICATION NUMBER: 60/051,705
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 34
LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

Query Match 100.0%; Score 43; DB 4; Length 3634;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 43
Db 2812 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 2854

RESULT 6
PCT-US95-12987-1
Sequence 1, Application PC/TUS9512987
GENERAL INFORMATION:
APPLICANT: LAFEMINA, R.
APPLICANT: SARANA, V.
APPLICANT: VELOSKI, C.
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROY D. MEREDITH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12987
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEREDITH, ROY D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 19262 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-12987-1

Query Match 48.8%; Score 21; DB 5; Length 771;
Best Local Similarity 73.0%; Pred. No. 9;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCAGTGGGCTTGA 37
Db 539 TCACACAGCGCTTCCAGAACTCAGCGGCGGCGGCGG 575

RESULT 7
PCT-US95-12987-3
Sequence 3, Application PC/TUS9512987
GENERAL INFORMATION:
APPLICANT: LAFEMINA, R.
APPLICANT: SARANA, V.
APPLICANT: VELOSKI, C.
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROY D. MEREDITH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA

ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12987
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEREDITH, ROY D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 19262 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-12987-3

Query Match 48.8%; Score 21; DB 5; Length 771;
Best Local Similarity 73.0%; Pred. No. 9;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TCAACTGGGGCTCCAGACTCAGTGGGCTACAG 37
Db 539 TCACACAGCGGTTTCAGACCTCAGCGGCGGACCG 575

RESULT 8
PCT-US95-12987-5
Sequence 5, Application PC/TUS9512987
GENERAL INFORMATION:
APPLICANT: LAPEMINA, R.
APPLICANT: SARANA, V.
APPLICANT: VELOSKI, C.
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROY D. MEREDITH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12987
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEREDITH, ROY D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: 19262 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4678
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-12987-5

Query Match 48.8%; Score 21; DB 5; Length 771;
Best Local Similarity 73.0%; Pred. No. 9;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TCAACTGGGGCTCCAGACTCAGTGGGCTACAG 37
Db 539 TCACACAGCGGTTTCAGACCTCAGCGGCGGACCG 575

RESULT 9
US-08-409-731A-1
Sequence 1, Application US/08409731A
Patent No. 5658758
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 94..414
US-08-409-731A-1

Query Match 48.4%; Score 20.8; DB 1; Length 861;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 11 GCCTCCAGACTCAGTGGGCTTACAGCTTGG 42
Db 96 GCCTCCAGACTCAGTGGGCTTACAGCTTGG 127

RESULT 10
US-08-470-298B-1
Sequence 1, Application US/08470298B
Patent No. 5844081

GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,298B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PFI75D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 94..414
US-08-470-298B-1

Query Match 48.4%; Score 20.8; DB 2; Length 861;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 11 GCCTCCAGACTGCTGGGCGCTACAGCTTTG 42
DB 96 GCCTCCAGACTGCTGGGCGCTACAGCTTTG 127

RESULT 11
US-09-023-073A-1
Sequence 1, Application US/09023073A
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,073A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WALES, MICHELE M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PFI75D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 94..414
US-09-023-073A-1

Query Match 48.4%; Score 20.8; DB 2; Length 861;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 11 GCCTCCAGACTGCTGGGCGCTACAGCTTTG 42
DB 96 GCCTCCAGACTGCTGGGCGCTACAGCTTTG 127

RESULT 12
US-09-361-737-1
Sequence 1, Application US/09361737
Patent No. 6287812
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/023,073
APPLICATION NUMBER: 09/023,073
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: WALES, MICHELE M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PFI75D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 861 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 94..414
US-09-361-737-1

Query Match 48.4%; Score 20.8; DB 4; Length 861;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 11 GCCTCCAGAACTCACTGGGGCCTACAGCTTTG 42
||||| ||||||| ||| |||||
Db 96 GCCTCCACACCTCACTGGCTACTACCGCTTTG 127

RESULT 13

US-08-820-825-1
Sequence 1, Application US/08820825
Patent No. 5945309

GENERAL INFORMATION:

APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,825
FILING DATE: 19-MAR-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 944 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 94..498
US-08-820-825-1

Query Match 48.4%; Score 20.8; DB 2; Length 944;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 11 GCCTCCAGAACTCACTGGGGCCTACAGCTTTG 42
||||| ||||||| ||| |||||
Db 96 GCCTCCACACCTCACTGGCTACTACCGCTTTG 127

RESULT 14

US-09-307-817-1
Sequence 1, Application US/09307817
Patent No. 6232291

GENERAL INFORMATION:

APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,817
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,825
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF222
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 944 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 94..498
US-09-307-817-1

Query Match 48.4%; Score 20.8; DB 4; Length 944;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 11 GCCTCCAGAACTCACTGGGGCCTACAGCTTTG 42
||||| ||||||| ||| |||||
Db 96 GCCTCCACACCTCACTGGCTACTACCGCTTTG 127

RESULT 15

US-09-734-036-1
Sequence 1, Application US/09734036
Patent No. 6413726

GENERAL INFORMATION:

APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE

Query Match 48.4%; Score 20.8; DB 2; Length 944;
Best Local Similarity 78.1%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

1  STATE: MD
2  COUNTRY: USA
3  ZIP: 20850
4
5  COMPUTER READABLE FORM:
6  MEDIUM TYPE: Floppy disk
7  COMPUTER: IBM PC compatible
8  OPERATING SYSTEM: PC-DOS/MS-DOS
9  SOFTWARE: Patentin Release #1.0, Version #1.30
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/09/734,036
12 FILING DATE:
13 CLASSIFICATION:
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 09/307,817
16 FILING DATE:
17 ATTORNEY/AGENT INFORMATION:
18 NAME: BROOKES, ANDERS A.
19 REGISTRATION NUMBER: 36,373
20 REFERENCE/DOCKET NUMBER: PF222
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (301) 309-8504
23 TELEFAX: (301) 309-8512
24 INFORMATION FOR SEQ ID NO: 1:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 944 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: DNA (genomic)
31 FEATURE:
32 NAME/KEY: CDS
33 LOCATION: 94..498
34 US-09-734-036-1

```

Query Match	48.4%	Score 20.8	DB 4	Length 944
Best Local Similarity	78.1%	Pred. No. 11		
Matches	25	Conservative	0	Mismatches 7; Indels 0; Gaps 0
OY	11	GCCTCCAGAACTCACTGGGCGCTACAGCTTGG	42	
Db	96	GCCTCCAGAACTCACTGGCTACTACGCGCTTGG	127	

Search completed: July 1, 2003, 22:12:42
Job time : 21.7687 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 20:48:50 ; Search time 56.7483 Seconds

(without alignments)
1124.814 Million cell updates/sec

Title: US-09-801-371A-2

Perfect score: 43
Sequence: 1 tcaactggggcctccagaa.....actggggcctacagcttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1055720 seqs, 742224136 residues

Total number of hits satisfying chosen parameters: 2111440

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	43	100.0	43	US-09-801-371A-2	Sequence 2, Appl1
2	43	100.0	43	US-09-801-371A-6	Sequence 6, Appl1
3	43	100.0	50	US-09-801-371A-8	Sequence 8, Appl1
4	43	100.0	81	US-09-801-371A-7	Sequence 7, Appl1
5	43	100.0	104	US-09-801-371A-1	Sequence 1, Appl1
6	43	100.0	104	US-09-801-371A-5	Sequence 5, Appl1
7	43	100.0	1643	US-10-218-547-3	Sequence 3, Appl1
8	43	100.0	1643	US-10-272-411-4	Sequence 4, Appl1
9	43	100.0	1643	US-10-272-411-4	Sequence 4, Appl1
10	43	100.0	3634	US-09-824-3228-1	Sequence 1, Appl1
11	43	100.0	3634	US-09-932-300-34	Sequence 34, Appl1
12	35	81.4	418	US-09-796-692-6223	Sequence 6223, Ap
13	35	81.4	418	US-10-040-862-6223	Sequence 6223, Ap
14	30.6	71.2	51	US-09-801-371A-10	Sequence 10, Appl
15	23	53.5	260	US-09-535-459-1127	Sequence 1127, Ap
16	22.2	51.6	27	US-09-801-371A-11	Sequence 11, Appl
17	22	51.2	363	US-09-783-590-10563	Sequence 10563, A
18	21.4	49.8	406	US-09-560-863-146	Sequence 146, App
19	21.4	49.8	1274	US-09-981-876-72	Sequence 72, Appl

C	20	21.4	49.8	1274	9	US-09-148-545-72	Sequence 72, Appl
C	21	21.4	49.8	1296	9	US-09-981-876-126	Sequence 126, App
C	22	21.4	49.8	1296	9	US-09-148-545-126	Sequence 126, App
C	23	21.4	49.8	1343	10	US-09-925-300-779	Sequence 779, App
C	24	21.4	49.8	3113	9	US-09-764-891-5580	Sequence 5580, Ap
C	25	21.4	49.8	24707	9	US-10-274-968-3	Sequence 3, Appl1
C	26	21.4	49.8	24707	10	US-09-740-027-3	Sequence 3, Appl1
C	27	21	49.8	768	9	US-10-214-932-97	Sequence 97, Appl
C	28	20.8	48.4	426	9	US-09-918-995-5224	Sequence 5224, Ap
C	29	20.8	48.4	461	9	US-09-918-995-15882	Sequence 15882, A
C	30	20.8	48.4	433	10	US-09-783-149-4012	Sequence 4012, Ap
C	31	20.8	48.4	551	10	US-09-737-149-13	Sequence 13, Appl
C	32	20.8	48.4	557	10	US-09-833-381-551	Sequence 551, Appl
C	33	20.8	48.4	817	10	US-09-737-149-15	Sequence 15, Appl
C	34	20.8	48.4	861	10	US-09-901-436A-1	Sequence 1, Appl1
C	35	20.8	48.4	944	12	US-10-153-740-1	Sequence 1, Appl1
C	36	20.8	48.4	957	9	US-10-032-366-2	Sequence 2, Appl1
C	37	20.8	48.4	1241	9	US-10-098-841-118	Sequence 118, App
C	38	20.8	48.4	1327	9	US-09-833-381-1346	Sequence 1346, Ap
C	39	20.8	48.4	65042	9	US-10-229-124-3	Sequence 3, Appl1
C	40	20.8	48.4	143306	10	US-09-729-920-3	Sequence 3, Appl1
C	41	20.4	47.4	239	10	US-09-998-590-1944	Sequence 1944, Ap
C	42	20.4	47.4	374	9	US-10-046-935-438	Sequence 438, App
C	43	20.4	47.4	374	9	US-09-878-178-438	Sequence 438, App
C	44	20.4	47.4	374	9	US-10-146-502-438	Sequence 438, App
C	45	20.4	47.4	493	10	US-09-864-761-5346	Sequence 5346, Ap

ALIGNMENTS

RESULT 1
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Jarrons, Farhat
; APPLICANT: Jarrons, Nayef
; APPLICANT: Ben-Assouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2
Query Match 100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TCAACTGGGGCCTCCAGAACTCAGTGGGCTACAGCTTTGA 43
Db 1 TCAACTGGGGCCTCCAGAACTCAGTGGGCTACAGCTTTGA 43
RESULT 2
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrons, Nayef
; APPLICANT: Ben-Assouli, Yitzhak

```

; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 43;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 43
DB 43 TCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 1

RESULT 3
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 50;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 43
DB 5 UCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 47

RESULT 4
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
```

```

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 81;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 43
DB 9 UCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 51

RESULT 5
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 104;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 43
DB 5 TCAAACTGGGGCCTCCAGACTGAGGCGCTTACAGCTTTGA 47

RESULT 6
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5
```

Query Match 100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 43
Db 100 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 58

RESULT 7
US-10-218-547-3
Sequence 3, Application US/10218547
Publication No. US20030100074A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
FILE REFERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/312,542
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/330,761
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1643
TYPE: DNA
ORGANISM: human
US-10-218-547-3

Query Match 100.0%; Score 43; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 43
Db 1074 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 1116

RESULT 8
US-10-272-411-4
Sequence 4, Application US/10272411
Publication No. US20030100068A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIRICS AND USES THEREOF
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1643
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ X01394.1
DATABASE ENTRY DATE: 1995-03-21
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
DATABASE ENTRY DATE: 2002-05-01
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ M35592.1

DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
DATABASE ENTRY DATE: 2002-08-01
RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match 100.0%; Score 43; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 43
Db 1074 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 1116

RESULT 9
US-10-272-328A-4
Sequence 4, Application US/10272328A
Publication No. US20030109444A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIRICS AND USES THEREOF
FILE REFERENCE: 60019620-0206
CURRENT APPLICATION NUMBER: US/10/272,328A
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 1643
TYPE: DNA
ORGANISM: Homo sapiens
US-10-272-328A-4

Query Match 100.0%; Score 43; DB 9; Length 1643;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 43
Db 1074 TCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTGA 1116

RESULT 10
US-09-824-322B-1
Sequence 1, Application US/09824322B
Publication No. US20030022848A1
GENERAL INFORMATION:
APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-
FILE REFERENCE: ISPH-0501
CURRENT APPLICATION NUMBER: US/09/824,322B
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 09/313,932
PRIOR FILING DATE: 1999-05-18
PRIOR APPLICATION NUMBER: US 09/166,186
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 503
SEQ ID NO 1
LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: CDS
LOCATION: 1796..981,1589..1634,1822..1869,2171..2592)
NAME/KEY: exon
LOCATION: (615)..(981)
NAME/KEY: Intron
LOCATION: (982)..(1588)
NAME/KEY: exon
LOCATION: (1589)..(1634)
NAME/KEY: Intron
LOCATION: (1635)..(1821)
NAME/KEY: exon
LOCATION: (1822)..(1869)
NAME/KEY: Intron
LOCATION: (1870)..(2070)
NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakauchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
US-09-824-322B-1

Query Match 100.0%; Score 43; DB 9; Length 3634;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGACTGAGCTGAGCTTGA 43

DB 2812 TCAAACTGGGGCCTCCAGACTGAGCTGAGCTTGA 2854

RESULT 11

US-09-932-300-34

Sequence 34, Application US/09932300

Publication No. US20030032788A1

GENERAL INFORMATION:

APPLICANT: GARVER, Eric

APPLICANT: TU, Guang-Chou

APPLICANT: ISRAEL, Yedy

TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION

FILE REFERENCE: 9855-302

CURRENT APPLICATION NUMBER: US/09/932,300

CURRENT FILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: US 60/051,705

PRIOR FILING DATE: 1997-07-03

PRIOR APPLICATION NUMBER: US 09/109,663

PRIOR FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 111

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 34

LENGTH: 3634

TYPE: DNA

ORGANISM: Homo sapiens

US-09-932-300-34

Query Match 100.0%; Score 43; DB 9; Length 3634;

Best Local Similarity 100.0%; Pred. No. 2.4e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGACTGAGCTGAGCTTGA 43
DB 2812 TCAAACTGGGGCCTCCAGACTGAGCTGAGCTTGA 2854

RESULT 12

US-09-796-692-6223

Sequence 6223, Application US/09796692

Publication No. US20020198362A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796,692

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 9597

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6223

LENGTH: 418

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure

LOCATION: (1)

OTHER INFORMATION: n=A,T,C or G

US-09-796-692-6223

Query Match 81.4%; Score 35; DB 9; Length 418;

Best Local Similarity 88.4%; Pred. No. 4.4e-05;

Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGACTGAGCTGAGCTTGA 43

DB 330 TCAAACTGGGGCCTCCAGACTGAGCTGAGCTTGA 372

RESULT 13

US-10-040-862-6223

Sequence 6223, Application US/10040862

Publication No. US20030078396A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Retter, Marc

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 6223
LENGTH: 418
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (1)
OTHER INFORMATION: n-A,T,C or G
US-10-040-862-6223

Query Match 81.4%; Score 35; DB 9; Length 418;
Best Local Similarity 88.4%; Pred. No. 4.4e-05;
Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCCTCAGAACTCAGTGGGGCTTGA 43
DB 330 TCAACTGGGGCCTCAGAACTCAGTGGGGCTTGA 372

RESULT 14
US-09-801-371a-10
Sequence 10, Application US/09801371A
Patent No. US20020155569A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
FILE REFERENCE: AA4084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 51
TYPE: RNA

ORGANISM: Oryctolagus cuniculus
US-09-801-371a-10

Query Match 71.2%; Score 30.6; DB 9; Length 51;
Best Local Similarity 73.0%; Pred. No. 0.0027;
Matches 27; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCCTCAGAACTCAGTGGGGCTTGA 37
DB 5 UCAACUGAGGCUCCAGACUCCUGGGCCUCCAG 41

RESULT 15
US-09-535-459-1127
Sequence 1127, Application US/09535459
Publication No. US20030040615A1
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullaly, Sara J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLEC
FILE REFERENCE: PD-1014 CIP
CURRENT APPLICATION NUMBER: US/09/535,459
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2170
SOFTWARE: PERL Program
SEQ ID NO 1127
LENGTH: 260
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID NO. US20030040615A1 hu00352946
US-09-535-459-1127

Query Match 53.5%; Score 23; DB 9; Length 260;
Best Local Similarity 74.4%; Pred. No. 3.4;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAACTGGGGCCTCAGAACTCAGTGGGGCTTGA 39
DB 201 TCATTGGGGGTCCAGAGCCACTGGGGCTTGA 239

Search completed: July 1, 2003, 22:16:15
Job time : 58.7483 secs

THIS PAGE BLANK (USPTO)